

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:24:41 ; Search time 300 Seconds
(without alignments)
1476.942 Million cell updates/sec

Title: US-10-713-648A-63

Sequence score: 2534
1 MSSSATVPLVPLAYGNTSASV.....GENTYDTKXGSDAAVAVTVV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2.*
1: UniProt_sprot.*
2: UniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2527	99.7	479	2	Q851M9_ORYSA	Q851M9 oryza sativ
2	2216	87.5	470	2	Q6T8L6_WHEAT	Q6T8L6 triticum ae
3	1991.5	78.6	498	2	Q84KJ6_ORYSA	Q84KJ6 oryza sativ
4	1889	74.5	480	2	Q69T29_ORYSA	Q69T29 oryza sativ
5	1871.5	73.9	486	2	Q93X02_ORYSA	Q93X02 lotus japon
6	1861	73.4	494	2	Q8H251_MEDTR	Q8H251 medicago tr
7	1715.5	67.7	497	2	Q8S2J3_ORYSA	Q8S2J3 oryza sativ
8	1714	67.6	486	2	Q84KJ7_ORYSA	Q84KJ7 oryza sativ
9	1714	67.6	486	2	Q8S2J3_ORYSA	Q8S2J3 oryza sativ
10	1687.5	66.6	497	2	Q8S2J3_ORYSA	Q8S2J3 oryza sativ
11	1682.5	66.4	475	1	AMT2_ARATH	Q9M67 arabiopsis
12	1436	56.7	458	2	Q2QY79_ORYSA	Q2QY79 oryza sativ
13	1297	51.2	359	2	Q3EBK4_ARATH	Q3EBK4 arabidopsis
14	1030	40.6	326	2	Q2RBN4_ORYSA	Q2RBN4 oryza sativ
15	1023.5	40.4	518	2	Q974J8_SULFO	Q974J8 sulfolobus
16	992.5	39.2	492	2	Q4JAD2_SULFO	Q4JAD2 sulfolobus
17	985.5	38.9	509	2	Q972J5_SULFO	Q972J5 sulfolobus
18	930.5	36.7	465	2	Q41R28_FERAC	Q41R28 ferriplasma
19	912.5	36.0	432	2	Q6KZ06_PICTO	Q6KZ06 picophyllus
20	722	28.5	412	1	Y663_METTH	Q72G98 methanobact
21	720.5	28.4	446	2	Q9HTX7_PSEAE	Q9HTX7 thermus the
22	717.5	28.3	442	2	Q5SM87_THERM	Q5SM87 thermus the
23	709.5	28.0	299	2	Q8W300_ORYSA	Q8W300 oryza sativ
24	708.5	28.0	299	1	AMT_AQUAE	Q66535 aquifex aeo
25	706	27.9	423	1	Q7MA87_WOLSU	Q7MA87 wolfinella s
26	697	27.5	437	2	Q3RYC8_RALME	Q3RYC8 ralstonia m
27	695.5	27.4	510	2	Q5P470_AZOSE	Q5P470 azoarcus sp
28	694	27.4	450	2	Q2NGJ2_9EURY	Q2NGJ2 methanospa
29	693.5	27.3	445	2	Q88B15_PSEEM	Q88B15 pseudomonas
30	692.5	27.3	445	2	Q50B00_PSEUD	Q50B00 pseudomonas
31	691.5	27.3	445	2	Q50B00_PSEUD	Q50B00 pseudomonas

32	691	27.3	431	2	Q66DR9_YERPS	Q66DR9 yersteinia ps
33	691	27.3	431	2	Q8ZC80_YERPE	Q8ZC80 yersteinia pe
34	690.5	27.2	438	2	Q3AFY9_CARHZ	Q3AFY9 carboxydobh
35	690.5	27.2	445	2	Q4C008_PSE14	Q4C008 pseudomonas
36	683.5	27.0	434	2	Q3XAI2_MERFL	Q3XAI2 methylobact
37	681	26.9	436	2	Q8Y2J2_RALSO	Q8Y2J2 ralstonia s
38	681	26.9	438	2	Q3PB17_PARDP	Q3PB17 paracoccus
39	680	26.8	432	2	Q8RPM1_PSEST	Q8RPM1 pseudomonas
40	676.5	26.7	443	2	Q2XHU3_PSEPU	Q2XHU3 pseudomonas
41	676.5	26.7	443	2	Q88CE8_PSEPF	Q88CE8 pseudomonas
42	676.5	26.7	445	2	Q3K4R2_PSEPF	Q3K4R2 pseudomonas
43	676	26.7	468	2	Q8RP89_PRHOO	Q8RP89 azoarcus sp
44	676	26.7	513	2	Q476K9_RALEJ	Q476K9 ralstonia e
45	672.5	26.5	443	2	Q6ND36_RHOPA	Q6ND36 rhodospseudo

ALIGNMENTS

RESULT 1	ID	Q851M9_ORYSA	PRELIMINARY;	PRT;	479 AA.
AC	Q851M9;				
DT	01-JUN-2003,	integrated into UniProtKB/TrEMBL.			
DT	01-JUN-2003,	sequence version 1.			
DT	21-FEB-2006,	entry version 12.			
DE	Putative ammonium transporter.				
GN	Name=OSUNBA0042109.15;				
OS	Oryza sativa (japonica cultivar-group).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BDP clade;				
OC	Ehrhartoideae; Oryzaceae; Oryza.				
OX	NCBI_TaxID=3947;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,				
RA	Overtton II L.L., Tseltrin T., Kim M.M., Bera J.J., Jin S.S.,				
RA	Padrosh D.W., Tallon L.U., Koo H., Ziemann V., Heiao J., Blunt S.,				
RA	Vanaken S.S., Riedmuller S.B., Peterback T.T., Feldlyum T.V.,				
RA	Yang Q.Q., Haas B.J., Sub B.B., Peterson J.J., Quackenbush J.,				
RA	White O., Salzberg S.L., Fraser C.M.;				
RT	Oryza sativa chromosome 3 BAC OSUNBA0042109 genomic sequence."				
RU	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
RU	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
RU	[2]				
RU	NUCLEOTIDE SEQUENCE.				
RU	Buell R.;				
RU	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.				
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CC	Distributed under the Creative Commons Attribution-NonDerivs license				
CC	EMBL; AC104487; AAC41130.1; -; Genomic_DNA.				
DR	Gramene; Q851M9; -				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0008519; F:ammonium transporter activity; IEA.				
DR	GO; GO:0008510; P:transport; IEA.				
DR	InterPro; IPR001905; Ammonium_transp.				
DR	InterPro; IPR010256; RH_like_transp.				
DR	InterPro; IPR002229; RhesusRD.				
DR	PANTHER; PTHR11730; Ammonium_transp; 1.				
DR	Pfam; PF00909; Ammonium_transp; 1.				
DR	PRINTS; PR00342; RHESUSRD.				
DR	TIGR; TIGR00836; amt; 1.				
DR	SEQUENCE 479 AA; 50853 MW; E9145C542F4664A5 CRC64;				
QY	Query Match	99.7%;	Score 2527;	DB 2;	Length 479;
QY	Best Local Similarity	99.6%;	Pred. No. 3.1e-178;		
QY	Matches 477;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
DB	1 MSSSATVPLVPLAYGNTSASVADMLNKGDNAWQVLAATVGLGSGVPLVVLVYGGVYKKKKA 60				
DB	1 MSSSATVPLVPLAYGNTSASVADMLNKGDNAWQVLAATVGLGSGVPLVVLVYGGVYKKKKA 60				

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QY 61 VNSAFMAALYAPAAWVICWVTWYNNNSFGSKLLPIWKGARPALDQGLVGRALPATVHR 120
DB 61 VNSAFMAALYAPAAWVICWVTWYNNNSFGSKLLPIWKGARPALDQGLVGRALPATVHR 120
QY 121 ADGSEVTAABVEPLYPMAIVVYFQCVPAATLLILVAGSLIGRMSFLAMMI FVPLMLTFSYT 180
DB 121 ADGSEVTAABVEPLYPMAIVVYFQCVPAATLLILVAGSLIGRMSFLAMMI FVPLMLTFSYT 180
QY 181 VAPAFSLMGGGFLFHWGVIDYCCGYVHVHAGTAGTAAVWGPBACRDERPPNNILFT 240
DB 181 VAPAFSLMGGGFLFHWGVIDYCCGYVHVHAGTAGTAAVWGPBACRDERPPNNILFT 240
QY 241 LTGAGLLMGMAGFNGGPGYAAANSVASMALVNTNICTAMSLIWTCLDVIFFPKKSVGA 300
DB 241 LTGAGLLMGMAGFNGGPGYAAANSVASMALVNTNICTAMSLIWTCLDVIFFPKKSVGA 300
QY 301 VOGMITGLVCITPPAGVVGMAALVWGLAGSI PWYTMWILHKRSKILQVDDTLGVFHT 360
DB 301 VOGMITGLVCITPPAGVVGMAALVWGLAGSI PWYTMWILHKRSKILQVDDTLGVFHT 360
QY 361 HGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQKQIAGGLFVWANNVAV 420
DB 361 HGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQKQIAGGLFVWANNVAV 420
QY 421 TSLICLAIMLVPLRMPDCKLEVGDDAVHGEBAVALMGDEMYDTYKHGSDAAVAPVV 479
DB 421 TSLICLAIMLVPLRMPDCKLEVGDDAVHGEBAVALMGDEMYDTYKHGSDAAVAPVV 479

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RESULT 2

OG6T86 WHEAT PRELIMINARY; PRT: 470 AA.

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AC 06T86 WHEAT PRELIMINARY; PRT: 470 AA.
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 8.
DE Ammonium transporter AMT2.1.
GN Name=AmT2.1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC Poaceae; Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhao X., Yang G., Tong Y., Li B., Miao J., Li Z.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AY428038, AAR87397.1; -, mRNA.
DR Gramene; Q6T8L6; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008119; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium_transp.
DR InterPro; IPR001734; Na/solute_transp.
DR InterPro; IPR010256; RH_like_transp.
DR InterPro; IPR002229; RhesusRD.
DR PANTHER; PTHR11730; Ammonium_transp; 1.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RhesusRD.
DR TIGRfam; TIGR00836; amc; 1.
DR PROSITE; PS00457; NA_SOLUTE_SYM_2; UNKNOWN 1.
SQ SEQUENCE 470 AA; 50056 MW; 96804C139DC46A38 CRC64;

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Query Match 87.5%; Score 2216; DB 2; Length 470;
 Best Local Similarity 86.0%; Pred. No. 2.9e-155;
 Matches 404; Conservative 30; Mismatches 34; Indels 2; Gaps 1;

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DB 3 VPVAYQNTSAAVADWLKNGDNAMQLTASTLVGLMSVPGMVTLYGGVKKKAVNSAFMA 62
QY 68 LYAFPAWVICWVTWYNNNSFGSKLLPIWKGARPALDQGLVGRALPATVHRADGSVET 127
DB 63 LYAFPAWVICWVTWYNNNSFGSKLLPIWKGARPALDQGLVGRALPATVHRADGSVET 122
QY 128 AAVEPLYPMAIVVYFQCVPAATLLILVAGSLIGRMSFLAMMI FVPLMLTFSYTGAFLW 187
DB 123 AMVEYFPMAIVVYFQCVPAATLLILVAGSLIGRMSFLAMMI FVPLMLTFSYTGAFLW 182
QY 188 GGGFLFHWGVIDYCCGYVHVHAGTAGTAAVWGPBACRDERPPNNILFTLTGALL 247
DB 183 GGGFLFHWGVIDYCCGYVHVHAGTAGTAAVWGPBACRDERPPNNILFTLTGALL 242
QY 248 WGMAGFNGGPGYAAANSVASMALVNTNICTAMSLIWTCLDVIFFPKKSVGA VOGMITG 307
DB 243 WGMAGFNGGPGYAAANSVASMALVNTNICTAMSLIWTCLDVIFFPKKSVGA VOGMITG 302
QY 308 LVCITPPAGVVGMAALVWGLAGSI PWYTMWILHKRSKILQVDDTLGVFHTGAGLL 367
DB 303 LVCITPPAGVVGMAALVWGLAGSI PWYTMWILHKRSKILQVDDTLGVFHTGAGLL 362
QY 368 GGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQKQIAGGLFVWANNVYTSILICA 427
DB 363 GGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQKQIAGGLFVWANNVYTSILICV 422
QY 428 INLVPLRMPDCKLEVGDDAVHGEBAVALMGDEMYDTYKHGSDAAVAPV 477
DB 423 INLVPLRMPDCKLEVGDDAVHGEBAVALMGDEMYDTYKHGSDAAVAPV 470

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RESULT 3

OG4KJ6 ORYZA PRELIMINARY; PRT: 498 AA.

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AC 084KJ6 ORYZA PRELIMINARY; PRT: 498 AA.
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ammonium transporter.
GN Name=OsAMT2;2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Root;
RC MEDLINE=22497958; PubMed=12610225; DOI=10.1093/pcp/pcg017;
RA Suenaga A., Moriya K., Sonoda Y., Ikeda A., von Weren N., Hayakawa T.,
RA Yamaguchi J., Yamaya T.;
RT "Constitutive expression of a novel-type ammonium transporter OsAMT2
in rice plants.";
RL Plant Cell Physiol. 44:206-211(2003).
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CC -----
EMBL: AB083582, BAC65232.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008119; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium_transp.
DR InterPro; IPR010256; RH_like_transp.
DR InterPro; IPR002229; RhesusRD.
DR PANTHER; PTHR11730; Ammonium_transp; 1.
DR Pfam; PF00909; Ammonium_transp; 1.
DR TIGRfam; TIGR00836; amc; 1.
DR PROSITE; PS01219; AMMONIUM_TRANSP; 1.
SQ SEQUENCE 498 AA; 53794 MW; 974AC5F13D05BFO CRC64;

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Query Match 78.6%; Score 1991.5; DB 2; Length 498;
 Best Local Similarity 75.6%; Pred. No. 1.2e-138;
 Matches 359; Conservative 53; Mismatches 56; Indels 7; Gaps 3;

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QY 1 MSSATVPLAYGNTSASVADMLKNDNAQOLVAATVGLQSPGLVYLGGVKKKNA 60
D 1 MSQDANMSVAYQPSGMA--VPEWLNKGDNAQOMISATLVQMSVGLVLYGSIYKKKNA 59
QY 61 VNSAFAPALFAFAVWICWWTAAVYNSFGEKLLPIWGKARPALDOGLLVGRALPATVHY- 119
D 60 VNSAFAPALFAFAVWICWWTAAVYNSFGEKLLPIWGKARPALDOGLLVGRALPATVHY 119
QY 120 ---RADGSVETAAVEPLYPMATVYVYFQCVAFAITLLVAGSLIGRMSFLAMMIFVPLML 175
D 120 KGGGADAVAVETPMVPLVYMAVMVYFQCVAFAITLLVAGSLIGRNNIKAMMLFVPLML 179
QY 176 TTSYTGATSLWGGGFLFHGVIDYCGGYIYHSAGIAGTAAVYWPRAQKRRPPN 235
D 180 TFSYTGATSLWGGGFLFHGVIDYCGGYIYHSAGIAGTAAVYWPRAQKRRPPN 239
QY 236 NILFTLTGAGLTMGNAGFNGGPRYANASVAMVNTNICTAMSLIWTCLDVIFPKK 295
D 240 NVLLMLTGAGLTMGNAGFNGGPRYANASVAMVNTNICTAMSLIWTCLDVIFPKK 299
QY 296 SVVGAVOGITGAVCTTPAGVVOGMAALVYVLAGSIPWTMMILHKRSKILQRYDDTL 355
D 300 SVIGAVOGMITGAVCTTPAGVVOGMAALVYVLAGSIPWTMMVYVHKSRLLQRYDDTL 359
QY 356 GVFTHTGAVGLGLLTGLFAEPTLCNLFVADSRGAFY-GGAGAQFGKQIAGLFPV 414
D 360 GVFTHTGAVGLGLLTGLFAEPTLCNLFVADSRGAFY-PGRGGIQLQFRVAGALFTI 419
QY 415 AMNVVYTSILCLAINLLVPLRMPDDKLEVGDDAVHGEAVALMGDEMDVYTKH 469
D 420 CMNVVYTSILCLAINLLVPLRMPDEELIGDDAVHGEAVALMGDEMDVYTKH 474

RESULT 4
Q69T29_ORYSA PRELIMINARY; PRT; 480 AA.
ID Q69T29_ORYSA PRELIMINARY; PRT; 480 AA.
AC Q69T29;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Putative ammonium transporter.
GN Name=P0451A10.33;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade;
OC Eriophytidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC
clone: P0451A10."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AP004775; BAD33268.1; -; Genomic_DNA.
D Gramene: Q69T29;
D GO: GO:0016020; C:membrane; IEA.
D GO: GO:0008519; F:ammonium transporter activity; IEA.
D GO: GO:0006810; P:transport; IEA.
D InterPro: IPR001905; Ammonium transp.
D InterPro: IPR010256; RH like transp.
D InterPro: IPR002229; RhoeusRD.
D PANTHER: PTHR11730; Ammonium transp.; 1.
D Pfam: PF00909; Ammonium transp.; 1.
D PRINTS: PR00342; RHESUSRD.
D TIGRfam: TIGR00836; amt; 1.
D PROSITE: PS01219; AMMONIUM TRANSP.; 1.
D SEQUENCE 480 AA; 51660 MW; 2964439DACSDA35 CRC64;

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Query Match 74.5%; Score 1889; DB 2; Length 480;
Best Local Similarity 72.0%; Pred No. 4.2e-131;
Matches 335; Conservative 62; Mismatches 66; Indels 2; Gaps 1;

QY 4 SATVPLAYGNTSASVADMLKNDNAQOLVAATVGLQSPGLVYLGGVKKKNA 63
D 2 AGAIFMAQ--TTBSPDMLKNDNAQOMTSATLVGLQSMGLVLYGSIYKKKNA 59
QY 64 AFMALFAFAVWICWWTAAVYNSFGEKLLPIWGKARPALDOGLLVGRALPATVHY 123
D 60 AFMALFAFAVWICWWTAAVYNSFGEKLLPIWGKARPALDOGLLVGRALPATVHY 119
QY 124 SVETAVERPLYPMATVYVYFQCVAFAITLLVAGSLIGRMSFLAMMIFVPLMLTFSYVGA 183
D 120 SAEAPMLKFLYPATVYVYFQCVAFAITLLVAGSLIGRNNIKAMMLFVPLMLTFSYVGA 179
QY 184 FSLMGGFLFHGVIDYCGGYIYHSAGIAGTAAVYWPRAQKRRPPNILETLTG 243
D 180 FSLMGGFLFHGVIDYCGGYIYHSAGIAGTAAVYWPRAQKRRPPNILETLTG 239
QY 244 AGLLMGNAGFNGGPRYANASVAMVNTNICTAMSLIWTCLDVIFPKKSVGAVOG 303
D 240 AGLLMGNAGFNGGPRYANASVAMVNTNICTAMSLIWTCLDVIFPKKSVGAVOG 299
QY 304 MTGAVCTTPAGVVOGMAALVYVLAGSIPWTMMILHKRSKILQRYDDTLGVFTHTG 363
D 300 MTGAVCTTPAGVVOGMAALVYVLAGSIPWTMMVYVHKSRLLQRYDDTLGVFTHTG 359
QY 364 AGLLGLLTGLFAEPTLCNLFVADSRGAFYGGAGAGQFGKQIAGLFPVAMNVVYSL 423
D 360 AGLLGLLTGLFAEPTLCNLFVADSRGAFYGGAGAGQFGKQIAGLFPVAMNVVYSL 419
QY 424 ICLAINLLVPLRMPDDKLEVGDDAVHGEAVALMGDEMDVYTKH 468
D 420 ICYIISLILPLRIADQELIGDDAVHGEAVALMGDEMDVYTKH 464

RESULT 5
Q93X02_LOTJA PRELIMINARY; PRT; 486 AA.
ID Q93X02_LOTJA PRELIMINARY; PRT; 486 AA.
AC Q93X02;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 14.
DE Putative ammonium transporter AMT2.
OS Lotus japonicus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Nitrogen-fixing nodules;
RT TISSUE=Nitrogen-fixing nodules;
RX MEDLINE=22490499; PubMed=12602894; DOI=10.1027/10222298;
RT Simon-Rosin U., Wood C., Urdavari M.K.;
RT "Molecular and cellular characterization of LjAMT2.1, an ammonium
transporter from the model legume Lotus japonicus."
RL Plant Mol. Biol. 51:99-108 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Nitrogen-fixing nodules;
RA Simon U., Urdavari M.K.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AF187962; AAL06212.1; -; mRNA.
D GO: GO:0016020; C:membrane; IEA.
D GO: GO:0008519; F:ammonium transporter activity; IEA.
D GO: GO:0006810; P:transport; IEA.
D InterPro: IPR001905; Ammonium transp.
D InterPro: IPR010256; RH like transp.

```

DR InterPro: IPR002229; RheusRHD.
DR PANTHER: PTHR11730; Ammonium_transpt; 1.
DR Pfam: PF00909; Ammonium_transp; 1.
DR PRINTS: PR00342; RHESUSRHD.
DR TIGRFAMs: TIGR00836; amc; 1.
DR PROSITE: PS01219; AMMONIUM_TRANSPT; 1.
DR SEQUENCE 486 AA; 52343 MW; 060E893849FA334D CRC64;

Query Match 73.9%; Score 1871.5; DB 2; Length 486;
Best Local Similarity 73.6%; Pred.No. 8.3e-130;
Matches 340; Conservative 49; Mismatches 72; Indels 1; Gaps 1;

QY 9 PLAYGNTSASVADMLKNGDNAMOLVAATLVGLQSVGLVVLVYGGVKKKMAVNSAFML 68
DB 4 PLAYGNTLPAS-PEMLNKGDNAHQMTAATLVGLQSMGLVILVASYIKKKMAVNSAFML 62
QY 69 YAFAAVMICVMTVAAYNMSFGEKLLPIWGKARPALDQGLVGRALPATVHYRADGSVETA 128
DB 63 YAFAAVLLCWLVCVRMARFGDKLPFWGKGAPALGQKFLINQASVDESHYFNNGSIETQ 122
QY 129 AVEPLYPNATVYVFCVPAITLILVAGSLGRMSFLAMNIFVPLMTFSYTVGAFSLMG 188
DB 123 TORPEYPAATLVYFQFNFAITMILLAGSVLGRMNIKAMMAFVPLMLTFSYTVGAFSLMG 182
QY 189 GGFLEPMGVIDYCGGYVILVHVSAGIAGFTAAVYWGPPRAQKDRERFPNNILFTLTGAGLLM 248
DB 183 GGFLEPMGVIDYCGGYVILVHVSAGIAGFTAAVYWGPPRAQKDRERFPNNILFTLTGAGLLM 242
QY 249 MGMAGFNGGPPYAANSVSAVAALNTNICTAMSLIWTCLDVIFFKKPSVYGAQGMITGL 308
DB 243 MGMAGFNGGAPYAANIDASIAVLNTNICATSLIWTSLDVAFFGKPSYIGAVQGMITGL 302
QY 309 VITTPAAGVQGMALVWGLAGSTPWTMTLHKRSKILQKVDPLGVFHTHAAGLLG 368
DB 303 VITTPAGAGVQGMALVWGLAGSTPWTMTLHKRSKILQKVDPLGVFHTHAAGLLG 362
QY 369 GLTGLFAEPTLCNLELPVADSRGAFYGGAGAGQFQKQIAGGLFVYAMVWVTSILCLAI 428
DB 363 GLTGLFAEPTLCNLELPVADSRGAFYGGAGAGQFQKQIAGGLFVYAMVWVTSILCLAI 422
QY 429 NLVPLRMPDDKLEVGDDAVHGEAAYALWGDGEMVDVTHGS 470
DB 423 NLVPLRMPDDKLEVGDDAVHGEAAYALWGDGEMVDVTHGS 464

RESULT 6
Q8H251_MEDTR PRELIMINARY; PRT; 494 AA.
ID Q8H251_MEDTR
AC Q8H251;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Amc2-like protein.
OS Medicago truncatula (Barrel medic).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosidae; eustosida I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
OC Medicago.
OX NCBI_TaxID=3880;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Peng J., Chen Y., Huang C.-H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
EMBL: AY122328; AAN06953.1; -; mRNA.
DR GO: GO:0016020; Cmembrane; IEA.
DR GO: GO:0008519; F:ammonium transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR001905; Ammonium_transpt.
DR InterPro: IPR010256; RH_like_transpt.

DR InterPro: IPR002229; RheusRHD.
DR PANTHER: PTHR11730; Ammonium_transpt; 1.
DR Pfam: PF00909; Ammonium_transp; 1.
DR PRINTS: PR00342; RHESUSRHD.
DR TIGRFAMs: TIGR00836; amc; 1.
DR PROSITE: PS01219; AMMONIUM_TRANSPT; 1.
DR SEQUENCE 494 AA; 53292 MW; D0F0816330ADD4F4 CRC64;

Query Match 73.4%; Score 1861; DB 2; Length 494;
Best Local Similarity 71.5%; Pred.No. 5e-129;
Matches 338; Conservative 55; Mismatches 74; Indels 6; Gaps 3;

QY 11 AYQNTSASVADMLKNGDNAMOLVAATLVGLQSVGLVVLVYGGVKKKMAVNSAFMALYA 70
DB 6 AYQNTLPAS-PEMLNKGDNAHQMTAATLVGLQSMGLVILVASYIKKKMAVNSAFMALYA 64
QY 71 FAAVMICVMTVAAYNMSFGEKLLPIWGKARPALDQGLVGRALPATVHYRADGS-VEFDA 129
DB 65 FAAVLLCWLVAAYRAFDGLLPFWGKGAPALGQKFLVABAKVPASTHYXKGVDETPM 124
QY 130 VEPLYPNATVYVFCVPAITLILVAGSLGRMSFLAMNIFVPLMTFSYTVGAFSLMG 189
DB 125 BEPPEPMASLVYFQFTFAITMILLAGSVLGRMNIKAMMAFVPLMLTFSYTVGAFSLMG 184
QY 190 GGFLEPMGVIDYCGGYVILVHVSAGIAGFTAAVYWGPPRAQKDRERFPNNILFTLTGAGLLM 249
DB 185 GGFLEPMGVIDYCGGYVILVHVSAGIAGFTAAVYWGPPRAQKDRERFPNNILFTLTGAGLLM 244
QY 250 MGMAGFNGGPPYAANSVSAVAALNTNICTAMSLIWTCLDVIFFKKPSVYGAQGMITGLV 309
DB 245 MGMAGFNGGAPYAANVASSIAVLNTNICATSLIWTSLDVAFFGKPSYIGAVQGMITGLV 304
QY 310 CITTPAAGVQGMALVWGLAGSTPWTMTLHKRSKILQKVDPLGVFHTHAAGLLG 369
DB 305 CITTPAGAGVQGMALVWGLAGSTPWTMTLHKRSKILQKVDPLGVFHTHAAGLLG 364
QY 370 LITGLFAEPTLCNLELPVADSRGAFYGGAGAGQFQKQIAGGLFVYAMVWVTSILCLAI 429
DB 365 LITGLFAEPTLCNLELPVADSRGAFYGGAGAGQFQKQIAGGLFVYAMVWVTSILCLAI 424
QY 430 NLVPLRMPDDKLEVGDDAVHGEAAYALWGDGEMVDVTHGS---DAAVAPV 478
DB 425 NLVPLRMPDDKLEVGDDAVHGEAAYALWGDGEMVDVTHGS---DAAVAPV 477

RESULT 7
Q8S233_ORYSA PRELIMINARY; PRT; 497 AA.
ID Q8S233_ORYSA
AC Q8S233;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Putative ammonium transporter.
GN Name=P044604.35;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade;
OC Eriactoidae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Karayose Y.,
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hishida S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Nachita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,

RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.,
RT "The genome sequence and structure of rice chromosome 1.",
RL Nature 420:312-316(2002).
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DR EMBL; AP003252; BAB89595.1; -, Genomic_DNA.
DR Gramene; O88233; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium_transp.
DR InterPro; IPR010256; RH like_transp.
DR InterPro; IPR002229; RheusRD.
DR PANTHER; PTHR11730; Ammonium_transp; 1.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHEUSRD.
DR TIGRfam; TIGR00836; amc; 1.
DR PROSITE; PS01219; AMMONIUM_TRANSNP; 1.
SQ SEQUENCE 497 AA; 52766 MW; 176574394D0D4DA7 CRC64;

Query Match 67.7%; Score 1715.5; DB 2; Length 497;
Best Local Similarity 69.3%; Pred. No. 2.8e-118;
Matches 312; Conservative 54; Mismatches 83; Indels 1; Gaps 1;

QY 19 SVADMLKNGDNAMQVLVAATLVGSLGVSFGLVVLVYGVVKKKMAVSAFMAVYAAVWICW 78
DB 16 AVFEMLTGNGQQLAAATFVGLQSMGLVVLVGSIVYKKKMAVSAFMAVYAAVSTLIW 75
QY 79 VYMAVMSFGEKLLPIWGKARPALDQGLVGRALPATVHYRADSVETAAVEPLYPMAT 138
DB 76 VLVGFMAFGDRLPFMGKAGALTTEGFLVARASVPATAHYGDKGALLESPTPEYPEAS 135
QY 139 VYVFGCVPAITLLVAGSLIGRMSFLAMMIFVPLMTFSTYTGAFSLMGCGFLPHKGV 198
DB 136 MVLFQELAAITLVLLAGSLIGRNTIKAMWAFPLMLTFSTYTCAPSLMGCGFLYQGV 195
QY 199 DYCGGVYIHVSAGIAGFTAAVYVGPRAQKDERFPNNILFTLTGAGLLMMGAFNGCG 258
DB 196 DYCGGVYIHSSGIAGFTAAVYVGPRAKDERFPNNILMTAGGLLMMGAFNGCGA 255
QY 259 PYAANSVAMAVLNTNI CTAMSLIWTCLDVIFFKRSVVGAVGMITGLVCTTPAAGV 318
DB 256 PYAPNITASIAVANTVNSAASLLTWTCLDVIFFKRSVIGAVQGMWTLVCTTPAGLV 315
QY 319 QGAAALVGVLAISIPYTMIIHKRSKILQRYDDTLGVHTGAVAGLLTGLFAEP 378
DB 316 HTMAALIMGCGSLPFWMMIHKRSALIQYDDTLAVPHTAAVAGLLGGLTGLFALP 375
QY 379 TLGNLFLPVADSRGAFYGAAGAFQKQIAGLFVAVANNVVTSLCIAINLVPLRMPD 438
DB 376 DLAAVHTHTGAGAFYGG-GIAQVGKQIAGLFFVAVANNVATVILLGVLVPLRMPD 434
QY 439 DKLEVGDDAVHGEAYALMGDGEYDVTYK 468
DB 435 EQLKIGDDAHGEAYALMGDERFDVTRH 464

RESULT 8
Q84K95_ORYSA PRELIMINARY; PRT; 486 AA.
AC Q84K95;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Ammonium transporter.
GN Name=OsAMT2;1;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

OC Eriharoidae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NOBLEOTIDE SEQUENCE.
RC TISSUE=Roots;
RX MEDLINE=22497958; PubMed=12610225; DOI=10.1093/pcp/pcg017;
RA Suenaga A., Moriya K., Sonoda Y., Ikeda A., von Widen N., Hayakawa T.,
RA Yamaguchi J., Yamaya T.;
RT "Constitutive expression of a novel-type ammonium transporter OsAMT2
in rice plants.",
RL Plant Cell Physiol. 44:206-211(2003).
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DR EMBL; AB051864; BAB87832.1; -, mRNA.
DR Gramene; O84K95; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium_transp.
DR InterPro; IPR010256; RH like_transp.
DR InterPro; IPR002229; RheusRD.
DR PANTHER; PTHR11730; Ammonium_transp; 1.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHEUSRD.
DR TIGRfam; TIGR00836; amc; 1.
DR PROSITE; PS01219; AMMONIUM_TRANSNP; 1.
SQ SEQUENCE 486 AA; 51411 MW; D70842P292B8CB7E7 CRC64;

Query Match 67.6%; Score 1714; DB 2; Length 486;
Best Local Similarity 69.0%; Pred. No. 3.5e-118;
Matches 319; Conservative 51; Mismatches 82; Indels 10; Gaps 4;

QY 10 LAYQNTSAS--VADMLKNGDNAMQVLVAATLVGSLGVSFGLVVLVYGVVKKKMAVSAFMA 66
DB 1 MAAAGVYSALPVPDMLKNGDNAMQVLTASTLVGISMGLVVLVGSIVYKKKMAVSAFMA 60
QY 67 ALYFAAVMICVYMAVMSFGEKLLPIWGKARPALDQGLVGRALPATVHYRADGSVE 126
DB 61 ALYFAVSSLLVWLVGFMAFGDQLPFMGKAGVALTOSYLVGRALPATVH---GAT- 115
QY 127 TAAVEPLYMATVYVQCVPAITLLVAGSLIGRMSFLAMMIFVPLMTFSTYTGAFSL 186
DB 116 -PTEFPYPAITLVLFQEPAAITLVLLAGSLVGRNTIKAMWAFPLMLTSTTVGAFL 174
QY 187 WGGGFLEHNGVIDYCGGVYIHVSAGIAGFTAAVYVGPRAQKDERFPNNILFTLTGAG 246
DB 175 WGGGFLEHNGVIDYCGGVYIHSSGIAGFTAAVYVGPRAKDERFPNNILMTAGGGL 234
QY 247 LMMGAFNGCGGYAANSVAMAVLNTNI CTAMSLIWTCLDVIFFKRSVVGAVGMIT 306
DB 235 LMMGAFNGCGAPYANIASVAVLNTNCAATSLMTCLDVIFFKRSVIGAVQGMW 294
QY 307 GLVCTTPAGVYVGMALVYAGSLIPYTMIIHKRSKILQRYDDTLGVHTGAVAG 366
DB 295 GLVCTTPAGVYVGMALVYAGSLIPYTMIIHKRSKILQRYDDTLGVHTGAVAG 354
QY 367 LGLLTLGLFAEPTLCNLFLPVADSRGAFYGAAGAFQKQIAGLFVAVANNVVTSLICT 426
DB 355 LGLLTLGLATPELFLSESTVPELGAFFGG-GIKRIGQLGAARVIAVMNVTTAILL 413
QY 427 AINLVPLRMPDDKLEVGDDAVHGEAYALMGDGEYDVTYK 468
DB 414 GIGLFLRMPDQQLMIGDDAHGEAYALMGDERFDVTRH 455

RESULT 9
Q84KJ7_ORYSA PRELIMINARY; PRT; 486 AA.
AC Q84KJ7;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.

DT 07-FEB-2006, entry version 12.
 DE Ammonium transporter.
 GN Name=OsAMT2; Synonyms=OJ1058_C01.9;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Eriaristidae; Oryzaceae; Oryza.
 OC NCBI_Taxid=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Etioiated shoot;
 RX MEDLINE=22497958; PubMed=12610225; DOI=10.1093/pcp/pcg017;
 RA Suenaga A., Moriya K., Sonoda Y., Ikeda A., von Wiren N., Hayakawa T.,
 RA Yamaguchi J., Yamaya T.;
 RT "Constitutive expression of a novel-type ammonium transporter OsAMT2
 in rice plants."
 RL Plant Cell Physiol. 44:206-211(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Chow T.-Y., Heing Y.-I. C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Liu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC EMBL, AB083581, BAC65231.1; -; Genomic DNA.
 DR EMBL, AC12159, AAT74008.1; -; Genomic DNA.
 DR Gramene, Q84KJ7;
 DR GO, GO:0016020; C:membrane, IEA.
 DR GO, GO:0008519; F:ammonium transporter activity, IEA.
 DR GO, GO:0006810; P:transport, IEA.
 DR InterPro: IPR001905; Ammonium transp.
 DR InterPro: IPR010256; RH like transp.
 DR InterPro: IPR002229; RheusRHD.
 DR PANTHER: PTHR11730; Ammonium transp.; 1.
 DR Pfam: PF00909; Ammonium transp.; 1.
 DR PRINTS: PR00342; RHESUSRHD.
 DR TIGRFAMs: TIGR00836; amc; 1.
 DR PROSITE: PS01219; AMMONIUM TRANSP.; 1.
 SQ SEQUENCE 486 AA; 51411 MW; D70842B92B8CB7E7 CRC64;
 Query Match 67.6%; Score 1714; DB 2; Length 486;
 Best Local Similarity 69.0%; Pred. No. 3,5e-118;
 Matches 319; Conservative 51; Mismatches 82; Indels 10; Gaps 4;
 QY 10 LAYGNTSAS---VADWLKGDNAADLVATLVGLQSVGLVVLVYGVVKKKKAANSAM 66
 DB 1 MAAAGYSASLPAVPMLNKGDNAWQLTASTLVGISMPGLVVLVYGSIVKKKAANSAM 60
 QY 67 ALYAFAPAVVICWWTAYNMSFGEKLPINGKAPALDOGLVGRALPATVHRADSYE 126
 DB 61 ALYAYSSILWLVGFRAFDQGLPFGKAGVALTOSTVGRATLPATAH---GAL- 115
 QY 127 TAAVEBLYPMATVYVQCFVFAITLLLVAGSLGRMSFLAMMIFVBLMTFSYTVAGSL 186
 DB 116 -PRTEFFYEATLVLFQFEPAITLVLAGSVLGRNNIKAMWAFETMLLLSTYVGAFL 174
 QY 187 WGGGFLFHHGVLDYCGGYVIHVSAGTAGTAAVWGPRAOKRERPPNNILFTLTGAGL 246
 DB 175 WGGGFLYRGGVLDYSGGYVIHSSGAGTAAVWGPRLKSDRERSPPNNILMTAGGL 234
 QY 247 LMMGMAFGNGGPGYANVSAMVLTNTICTAMSLVWTCTLDVIFPKKSVVGAOGMIT 306
 DB 235 LMMGMAFGNGGPGYANVITAASAVLNTVCAATSLMTCTLDVIFPKKSVVGAOGMIT 294
 QY 307 GLVCITPAAGVVGMAALVWGLAGSI PMYTMMLHKRSKILQKRVDDTLGVFTHGAGL 366
 DB 295 GLVCITPAAGLVGTMAAVVWGI PAFGSVPWFTMMLHKRSKILMKVDTLAVFTHAVAGL 354

QY 367 LGGLTGFLFABPTLCNLFPLVADSRGAFYGGAGAGAFQKQIAGGLFVYANVVTSLTCL 426
 DB 335 LGGILTGLATPBLFSLSTYPGLRGAFYGG-GIKQIKQKQAGAAFYANLVTTALL 413
 QY 427 AINLVLPMPDCKLEVGDVAHGEAYALWGDSEMYDVTH 468
 DB 414 GIGLFIPLRMPDEQLMIGDDAAHGEAYALWGDSEKFDATH 455
 RESULT 10
 OS Oryza sativa (Japonica cultivar-group).
 GN Name=OsAMT2; Synonyms=OJ1058_C01.9;
 AC O8S230;
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 15.
 DE Putative ammonium transporter.
 GN Name=P046G04.40;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Eriaristidae; Oryzaceae; Oryza.
 OC NCBI_Taxid=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu Y., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanemori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijiishi S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Ito S., Ito T., Ito Y., Iwachi A., Kamiya K.,
 RA Katsawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Meihara T., Mizuno H., Mizudayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1."
 RL Nature 420:312-316(2002).
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 CC EMBL, AP003252; BAB89598.1; -; Genomic DNA.
 DR Gramene, Q8S230;
 DR GO, GO:0016020; C:membrane, IEA.
 DR GO, GO:0008519; F:ammonium transporter activity, IEA.
 DR GO, GO:0006810; P:transport, IEA.
 DR InterPro: IPR001905; Ammonium transp.
 DR InterPro: IPR010256; RH like transp.
 DR InterPro: IPR002229; RheusRHD.
 DR PANTHER: PTHR11730; Ammonium transp.; 1.
 DR Pfam: PF00909; Ammonium transp.; 1.
 DR PRINTS: PR00342; RHESUSRHD.
 DR TIGRFAMs: TIGR00836; amc; 1.
 DR PROSITE: PS01219; AMMONIUM TRANSP.; 1.
 SQ SEQUENCE 497 AA; 53202 MW; 909D3CF41508C93B CRC64;
 Query Match 66.6%; Score 1687.5; DB 2; Length 497;
 Best Local Similarity 67.7%; Pred. No. 3.3e-116;
 Matches 304; Conservative 54; Mismatches 90; Indels 1; Gaps 1;
 QY 19 SVADWLKNGDNAMQVLAATLVGLQSVGLVVLVYGVVKKKKAANSAPALVAFAPAVVICW 78
 DB 16 AVPAVLNKGDITMQLVAATLVGLQSMPLVVLVYGSIVKKKAANSAPALVYASTLIW 75
 QY 79 VTMAYNMSFGEKLPINGKAPALDOGLVGRALPATVHRADSYETAAVEBLYPMAT 138
 DB 76 VLVGFRMAFGDRLTLPFWAKAGPALTODLVGRVAVPATAHSGSDGTLTETPRTEPYAEA 135

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QY 139 VYFQCVPAATITLIVAGSLGRMSFLAMNIPVPLMTSTYTGAFSLMGGLFPHMGVY 198
DB 136 LVLFEEFEPAITLIVLAGSLGRMNIKAMMAFPPLMLFSYTGASLWGGGLYOMGYI 195
QY 199 DYCGGVYIHVSAGIAGFTAAVWGPRAQXDRERFPNNIIFLTLTGAGLMMGAGFNCGG 258
DB 196 DYSGGVYIHSSVAGFTAAVWGPRLKSDRERFSPNNILMIAGGLMLMGAGNCGA 255
QY 259 PYANASVAMAVLNTNICTAMSLIWTCLDVIFFPKKPSVVGAVQGNITGLVCTTPAAGV 318
DB 256 PYAPNVTATVAVLNTNVSATSLTWTCLDVIFFKPSVVGAVQGNITGLVCTTPGAGV 315
QY 319 OGMAALVGVLAGSIPTTMMIIHKRSKIIQVDDTLGVHTHGVAGLGLTGLPAEP 378
DB 316 HTWSAMLMGMFAGSVPMFTMMIIHKKSTPLMKYDDTLAVFHTAVAGLGLVLTGLAP 375
QY 379 TLGNLFLPVADSRGAFVGAAGAFGKQIAGLFFVAMNVTSLCLAINLLVPLRMPD 438
DB 376 ELGALDCCPLPNNMGVFI-GSGIGQLGKGLFVYVWMLIVTSAILLCTGLFPLRMSD 434
QY 439 DKLEVGDDAVHGEAYALMGDGENYDVTX 467
DB 435 DQLMIGDDAHGEBAYALMGDGEKFDVTR 463

RESULT 11
AMT2 ARATH STANDARD; PRT; 475 AA.
ID AMT2 ARATH
AC 09M6N7;
DT 26-JUL-2002. Integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004. sequence version 2.
DE 07-MAR-2006. entry version 34.
GN Ammonium transporter 2 (ATAMT2).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE AND CHARACTERIZATION.
RC STRAIN=cv. C24; TISSUE=Root;
RX MEDLINE=20141244; PubMed=10675553; DOI=10.1016/S0014-5793(00)01153-4;
RA Sohlankamp C., Shelden M.C., Howitt S.M., Uchard M.K.;
RT "Characterization of Arabidopsis ATAMT2, a novel ammonium transporter
in plants.";
RL FEBS Lett. 467:273-278 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;
RA Lin X., Kaul S., Rounsley S.D., Shao T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rinning C.M., Koo H.L.,
RA Motil K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Taiton L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nieman W.C., White O., Eissen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768 (1999).
CC -!- FUNCTION: Transports ammonium, probably in an energy-dependent
manner. Does not transport methylammonium.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
(probable).
CC -!- TISSUE SPECIFICITY: Higher expression in shoots than roots.
CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)
family.
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CC -----
DR EMBL: AF182039.1:AAF37192.1; -; mRNA.
DR EMBL: AC003028; AAM14857.1; -; Genomic DNA.
DR F1R: T01260; T01260.
DR GenomeReviews; CT485783_GR; AT2G38290.
DR GeneFam; 3490; 317.
DR TAIR: At2g38290; -.
DR InterPro; IPR001905; Ammonium_transpt.
DR InterPro; IPR010256; RH_like_transpt.
DR InterPro; IPR002229; RheusRD.
DR PANTHER; PTHR11730; Ammonium_transpt; 1.
DR Pfam; PF00309; Ammonium_transp; 1.
DR PRINTS; PR00342; RHESUSRD.
DR TIGRPFAM; TIGR00836; ant; 1.
DR PROSITE; PS01219; AMMONIUM_TRANSP; 1.
DR Ammonia_transport; Membrane; Polymorphism; Transmembrane; Transport.
KW CHAIN 1
FT 1 475
FT TRANSMEM 27 47
FT TRANSMEM 55 75
FT TRANSMEM 120 140
FT TRANSMEM 148 168
FT TRANSMEM 183 203
FT TRANSMEM 218 238
FT TRANSMEM 254 274
FT TRANSMEM 279 299
FT TRANSMEM 302 322
FT TRANSMEM 336 356
FT TRANSMEM 389 409
FT TRANSMEM 95 95
SQ SEQUENCE 475 AA; 50768 MW; A4958B0A8D2CAB60 CRC64;
D -> N (in strain: cv. C24).

Query Match 66.4%; Score 1682.5; DB 1; Length 475;
Best local Similarity 66.8%; Pred. No. 7.3e-116;
Matches 300; Conservative 61; Mismatches 77; Indels 11; Gaps 1;

QY 20 VADMINKGNAMQVLAATVGLQSVGLVVLVGGVYKKMAVNSAFMALYAPAAVVCWV 79
DB 12 VPEMLKGNAMQVLAATVGLQSVGLVVLVGGVYKKMAVNSAFMALYAPAAVVCWV 71
QY 80 TWANNSFGEKLPFWGKAPALDQGLVGRALPATVHYRADGSVETAAVEELYPMATV 139
DB 72 LICYKNAFEBELPFGKGGAPAFDQGLYLGQAKIP-----NSNVAPYPPMATL 120
QY 140 VYFQCVPAATITLIVAGSLGRMSFLAMNIPVPLMTSTYTGAFSLMGGLFPHMGVYD 199
DB 121 VYFQCVPAATITLIVAGSLGRMNIKAMMAFPPLMLFSYTGASLWGGGLYOMGYI 180
QY 200 YCGGVYIHVSAGIAGFTAAVWGPRAQXDRERFPNNIIFLTLTGAGLMMGAGFNCGG 259
DB 181 YSGGVYIHSSVAGFTAAVWGPRLKSDRERFSPNNILMIAGGLMLMGAGNCGA 240
QY 260 PYANASVAMAVLNTNICTAMSLIWTCLDVIFFPKKPSVVGAVQGNITGLVCTTPAAGV 319
DB 241 PYANLSTSLAVLNTNLSAATSLTWTCLDVIFFKPSVVGAVQGNITGLVCTTPAAGV 300
QY 320 GMAALVGVLAGSIPTTMMIIHKRSKIIQVDDTLGVHTHGVAGLGLTGLPAEP 379
DB 301 TWAAIIVGVSAGTAPWASMMIHKKSALLQKDDTLAVFHTAVAGLGLVLTGLAP 360
QY 380 LCNLFLPVADSRGAFVGAAGAFGKQIAGLFFVAMNVTSLCLAINLLVPLRMPD 439
DB 361 LCVLVLPLPATRGAFFGNGKQLKQGLGAAPFAVWNVSTIILALRVFPLRMAE 420
QY 440 KLEVGDDAVHGEAYALMGDGENYDVTX 468
DB 421 ELGIGDDAHGEBAYALMGDGEKFDVTR 449

RESULT 12
Q2QYV9 ORYSA PRELIMINARY; PRT; 458 AA.
ID Q2QYV9_ORYSA
AC Q2QYV9;

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DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE Ammonium transporter family.
 GN ORFNames=LOC_Os12g01420;
 OS *Oryza sativa* (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BPP clade;
 OC Ehrhartoideae; Oryzaceae; *Oryza*.
 NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Wang R.A., McCombie W.A., Ouyang S.;
 RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: DP000011; ABA95601.1; -; Genomic DNA.
 DR SQA SEQUENCE 458 AA; 48077 MW; 3B2CAG65204BF2A CRC64;
 Query Match 56.7%; Score 1436; DB 2; Length 458;
 Best Local Similarity 59.4%; Pred. No. 1.1e-97;
 Matches 262; Conservative 73; Mismatches 98; Indels 8; Gaps 3;
 QY 17 SASVADMLKGNAMQVLAATLVGLQSVPGLVVLYGVGVKKKVAVNSAFMALYAPAAVMI 76
 DB 3 SVAVPEMLKGNAMQVLAATLVGLQSVPGLVVLYGVGVKKKVAVNSAFMALYAPAAVMI 62
 QY 77 CWVTAAYNNSFGEKLLPIWGKARPALDQGLVGRALPATVHYRADSVETAABEELPYM 136
 DB 63 CALMAHNNNAFGHRLPFVGRAPALAQHYMLTQALLPFTLHLSNGEVETAAPALYPS 122
 QY 137 AVVVVYQCPAATLTLVAGSLGRMSFLAMMIFVPLMLTFTSVAFSLMGSGFLFHNG 196
 DB 123 ASMVEFQMSAGVTGLVAGVAGVGRMSVYKMAAFVPLMTLSTVGAYSIWGGFLFHNG 182
 QY 197 VIDYCGGVYIVHSAGIAGFTAAVYVGPRAQKDERFPP--NNILFTLGTAGLLMGMAGFN 254
 DB 183 VMDYSGGVYVHLAAGVSGTAAVYVGPRAKREBEEMTAGGNLVANVAGLLMGMAGFN 242
 QY 255 NGGGPYANSVASMALVNTNICTAMSLIWTCLDVIFFKPSVGAAGMGTGLVCTPAA 314
 DB 243 NGGDPFSANTDSVAVLNTNICTTTSILAMVCCDIAYRGRPSVGAAGMGTGLVCTPAA 302
 QY 315 AGVYQGMALVWGVLAGSIPWYTMILHKRSKILQVDDTLGVFHTHGYAGLLGLTGLF 374
 DB 303 AGLVQGMALVWGVLAGSIPWYTMILHKRSKILQVDDTLGVFHTHGYAGLLGLTGLF 357
 QY 375 PAEPTLCNLFPLPADSRGAFYGGAGAGQFQIAGGLFVAVANVVTSLICLAINLLVPLR 433
 DB 358 FAHPFTLCMDFLPTGSRGLVYGRAGGVYLVKQVAAALFVAVANVVAITSILVYVAAFP 417
 QY 434 LKMPDDKLEVGDDAVHGEAAY 454
 DB 418 LKMTDELLAGDIAVHGEQAY 438
 RESULT 13
 Q3EBK4 ARATH PRELIMINARY; PRT; 359 AA.
 AC Q3EBK4;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 4.
 DE Protein At2g38290.
 GN OrderedLocustNames=At2g38290;
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
 OC Rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.U., Barnesad M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.D., Ronning C.M., Koo H.U.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*."
 RL Nature 402:761-768 (1999).
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 CC -----
 DR TAIR: At2g38290; -.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0008519; F:ammonium transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR001505; Ammonium_transp.
 DR InterPro: IPR010256; RH_like_transp.
 DR Pfam: PF00909; Ammonium_transp; 1.
 DR PRINTS: PR00342; RHESUSRD.
 DR PROSITE: PS01219; AMMONIUM_TRANSNP; UNKNOWN 1.
 DR SQA SEQUENCE 359 AA; 38153 MW; DCE32F9D3D3815A9 CRC64;
 Query Match 51.2%; Score 1297; DB 2; Length 359;
 Best Local Similarity 68.5%; Pred. No. 1.7e-87;
 Matches 228; Conservative 50; Mismatches 55; Indels 0; Gaps 0;
 QY 136 MATVYVQCPAATLTLVAGSLGRMSFLAMMIFVPLMLTFTSVAFSLMGSGFLFHNG 195
 DB 1 NATLVYQCPAATLTLVAGSLGRMSFLAMMIFVPLMLTFTSVAFSLMGSGFLFHNG 60
 QY 196 GVIDYCGGVYIVHSAGIAGFTAAVYVGPRAQKDERFPPNNILFTLGTAGLLMGMAGFN 255
 DB 61 GVIDYSGGVYVHLAAGVSGTAAVYVGPRAKREBEEMTAGGNLVANVAGLLMGMAGFN 120
 QY 256 GGGPYANSVASMALVNTNICTAMSLIWTCLDVIFFKPSVGAAGMGTGLVCTPAA 315
 DB 121 GGAPYANULTSIVLNTNICTSLVMTLTVIFPKSPVGAAGMGTGLVCTPAA 180
 QY 316 GVVQGMALVWGVLAGSIPWYTMILHKRSKILQVDDTLGVFHTHGYAGLLGLTGLF 375
 DB 181 GLIQTMALIIIGVSGTAPWASMMIHKRSKILQVDDTLGVFHTHGYAGLLGLTGLF 240
 QY 376 PAEPTLCNLFPLPADSRGAFYGGAGAGQFQIAGGLFVAVANVVTSLICLAINLLVPLR 435
 DB 241 AHPDLCVLTPLPATRGAFYGGAGQFQIAGGLFVAVANVVTSLICLAINLLVPLR 300
 QY 436 MPDDKLEVGDDAVHGEAAYALMGDEMYDVTKH 468
 DB 301 MAEEELGIGDDPAHGEAAYALMGDEKEDPATRH 333
 RESULT 14
 Q2RBN4 ORYSA PRELIMINARY; PRT; 326 AA.
 AC Q2RBN4;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Ammonium transporter AMT2.1, putative.
 GN ORFNames=LOC_Os11g01410;
 OS *Oryza sativa* (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BPP clade;
 OC Ehrhartoideae; Oryzaceae; *Oryza*.
 NCBI_TaxID=39947;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: DP000010; AB91064.1; -; Genomic DNA.
 DR SQ SEQUENCE 326 AA; 34717 MW; D106D9F1A38C91D3 CRC64;
 Query Match 40.6%; Score 1030; DB 2; Length 326;
 Best Local Similarity 58.3%; Pred. No. 7.9e-68;
 Matches 183; Conservative 56; Mismatches 71; Indels 4; Gaps 1;
 QY 17 SASVADMLNKGDNAWOLVAATLVGLQSVPLVLYGVGVKKKVAVNSAFNALYAFAAVWI 76
 DB 3 SAAVPEMLNKGDNAWOLVAATLVGLQSVPLVLYGVGVKKKVAVNSAFNALYAFAAVWI 62
 QY 77 CWTVAVYNSFGEKLLPIWGKARPALDQGLVGRPALPATVHYRADGSVETAAVEPLYPM 136
 DB 63 CMALMAHNNMFAFGRRLLPFVGRPAALADYMLSCALLPSTLHRSNGEVETAAVAAPLYPS 122
 QY 137 AATVYQCVPAATLTLLVAGSLGRMSFLAMMI FVPLMTFSYTVGAFSLMGGLFHHWG 196
 DB 123 ASNVFFQWAFAGVTVGLVAGAVLGRMSVKAMMAFVPLMTLTSTVGAVSLMGGLFHHWG 182
 QY 197 VIVYCGGYVIVHVSAGIAGFTAAVWVGPRADKRRER---PPNNILFTLTGAGILMWGMA 252
 DB 183 VMYSGGYVLLAAGVSGYTRAAVWVGPRKREDEEEMATSGNLLVWVAGAILMMGMT 242
 QY 253 GENGSGPYAANSVASNAVINTNICTAMSLIVTCLDVIFPKPSVGVAVOGMITGLVCIT 312
 DB 243 GFEGGDPFSANTDSVAIVNTHICATTSIVAVWCDAVAVGRPSVGVAVOGMITGLVCIT 302
 QY 313 PAAGVVGMAALVM 326
 DB 303 PRSNIRYSFLVVI 316
 RESULT 15
 Q974J8_SULTO PRELIMINARY; PRT; 518 AA.
 AC Q974J8;
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE 518aa long hypothetical ammonium transporter.
 GN OrderedLocustNames=ST0661;
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA STRAIN=UCM 10545 / ?;
 RC MEDLINE=21456156; PubMed=11572479; DOI=10.1093/dnares/8.4.123;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S., Aikai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka Y., Kudo Y., Yamazaki J., Kushida N., Ogunchi A.,
 RA Aoki K., Maeda S., Yanagishi M., Nishimura M., Yamagishi A., Oshima T.,
 RA Kikuchi H.;
 RA "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";
 RL DNA Rep. 8:123-140(2001).
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 DR EMBL: BA000023; BAB5560.1; -; Genomic DNA.
 DR DR BioCyc: STOK111955:ST0661-MONOMER; -;
 DR GO: GO:0016020; C:membrane; IEA.

DR GO: GO:0008519; F:ammonium transporter activity; IEA.
 DR GO: GO:0005810; P:transport; IEA.
 DR InterPro: IPR001905; Ammonium_transpt.
 DR InterPro: IPR010256; RH_like_transpt.
 DR InterPro: IPR002229; RheusRHD.
 DR PANTHER: PTHR11730; Ammonium_transpt; 1.
 DR Pfam: PF00909; Ammonium_transp; 1.
 DR PRINTS: PR00342; RHEUSRHD.
 DR TIGRFAMs: TIGR00836; amc; 1.
 DR PROSITE: PS01219; AMMONIUM_TRANSP; 1.
 DR Complete proteome, Hypothetical protein.
 DR SQ SEQUENCE 518 AA; 55179 MW; 990E469463D68DBD CRC64;
 Query Match 40.4%; Score 1023.5; DB 2; Length 518;
 Best Local Similarity 47.9%; Pred. No. 3.8e-67;
 Matches 217; Conservative 66; Mismatches 145; Indels 25; Gaps 10;
 QY 10 LAYQNT---SASVADMLNKGDNAWOLVAATLVGLQSVPLVLYGVGVKKKVAVNSAF 65
 DB 51 LALENTADYPSAAVSWLDTGSMNMLTRATFVGLQSVGVALLYAGLSKKKVAVNSAL 110
 QY 66 MALYAPAAVVICWTVWAVYNSFGE-KLPIWGKARPALDQGLVGRPALPATV-HYRADG 123
 DB 111 MVEYAPAAVIVVWMMIAGVNAFGHPALLSING-----YGLI--GYPLPAMLGHYEASQ 161
 QY 124 SVETAAVEPL-YPMATVYVFCQVFAITLLVAGSLGRMSFLAMMI FVPLMTFSYTVG 182
 DB 162 TVFGPTGTVDI-PTSTYIFQVFAITVLLAGVLERMNEFAMMI FVPLMTSLVSPV 221
 QY 183 AFSLMGSGFLFHHGVIDYCGYVIVHVSAGIAGFTAAVWVGPRADKRRERPPNNILFTLT 242
 DB 222 AYVLPFGGMLNQLGAVDFSGGYIIVHDAGVGLAALALGRLASR-KLEAHSLLVLA 280
 QY 243 GAGILMWGAGFENGSGPYAANSVASNAVINTNICTAMSLIVTCLDVIFPKPSVGVAVO 302
 DB 281 GAGILMWGDFENGSGPYGATIDAAIAIVNINATVSAITVWMLDMAFKKPTLVGATS 340
 QY 303 GMTTGLVCTTPAAGVQGMALVMGVLASIPYTMILHRSKILQRYDDTLGVFHTG 362
 DB 341 GAITGLVAITTPAAGVNGWEAMLIIGASISIPWLSYKKEPRLK---VDDTLGVFHTG 396
 QY 363 VAGILGGLTGLFAEPTLGNLFLPVADSRGAFYGGAGAQFGKQIAGLFFVAVMNVVTS 422
 DB 397 IAGIVGGLTGVADPNVQYVDPFL--KGALYGNL--YQLGIQAAAANVVFYDPAIF 452
 QY 423 LICLAINLLVPLMPDDKLEVGDDAVHGEBAVA 455
 DB 453 GLIKLIGLFIPLQAPPDTLAIGDYAMHGEVAYS 485

Search completed: July 22, 2006, 03:32:58
 Job time : 304 secs

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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:33:11 ; Search time 50 Seconds
(without alignments)
838,543 Million cell updates/sec

Title: US-10-713-648A-63
Perfect score: 2534
Sequence: 1 MESSATVPLAYQGNISASV.....GEMVDTKKGSDAAVAVPVV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/1aa/5/COMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/1aa/6/COMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/1aa/7/COMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/1aa/H/COMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/1aa/PCTUS.COMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/1aa/RB.COMB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2216	87.5	470	2	US-10-033-109-14
2	1860.5	73.4	486	2	US-10-033-109-12
3	1715.5	67.7	497	2	US-10-033-109-10
4	717.5	28.3	455	2	US-09-252-991A-23745
5	641	25.3	439	2	US-09-489-039A-12960
6	639	25.0	433	2	US-09-543-681A-6105
7	634.5	25.2	430	2	US-09-328-352-5397
8	582	23.0	437	2	US-09-134-001C-3907
9	532	21.0	463	2	US-09-902-540-15324
10	506	20.0	499	2	US-09-487-558B-194
11	476	18.8	452	2	US-09-602-787A-398
12	474.5	18.7	492	2	US-09-487-558B-192
13	338.5	13.4	501	2	US-08-635-967-2
14	335	13.2	361	2	US-09-134-000C-5907
15	313.5	12.4	500	2	US-10-033-109-4
16	305	12.0	494	2	US-10-033-109-6
17	284	11.2	63	2	US-10-033-109-8
18	275	10.9	441	2	US-09-328-352-4217
19	260.5	10.3	434	2	US-09-252-991A-18525
20	244	9.6	175	2	US-09-248-796A-20751
21	233.5	9.2	223	2	US-09-107-532A-3674
22	232	9.2	185	2	US-09-602-787A-2
23	214	8.4	224	2	US-09-107-532A-4102
24	208	8.2	240	2	US-09-248-796A-20193
25	178.5	7.0	487	2	US-09-949-016-9649
26	176.5	7.0	418	2	US-09-949-016-7328

27	129	5.1	607	2	US-09-252-991A-26825	Sequence 26825, A
28	128.5	5.1	470	2	US-09-603-208A-246	Sequence 246, App
29	128	5.1	183	2	US-10-033-109-2	Sequence 2, App1
30	124	4.9	303	2	US-09-372-934-2	Sequence 2, App1
31	124	4.9	303	2	US-09-766-916-2	Sequence 2, App1
32	124	4.9	303	2	US-09-766-898-2	Sequence 2, App1
33	124	4.9	303	2	US-09-637-040C-2	Sequence 2, App1
34	124	4.9	303	2	US-10-306-249-2	Sequence 2, App1
35	124	4.9	303	3	US-10-306-247-2	Sequence 2, App1
36	122	4.8	886	2	US-09-902-540-11981	Sequence 11981, A
37	119.5	4.7	458	2	US-09-252-991A-27645	Sequence 27645, A
38	119	4.7	413	2	US-09-543-681A-5108	Sequence 5108, Ap
39	118	4.7	321	2	US-09-252-991A-31084	Sequence 31084, A
40	117.5	4.6	91	2	US-09-602-787A-4	Sequence 4, App1
41	116.5	4.6	315	2	US-09-252-991A-28791	Sequence 28791, A
42	116	4.6	548	2	US-09-328-352-6605	Sequence 6605, Ap
43	114.5	4.5	457	2	US-09-902-540-15123	Sequence 15123, A
44	114.5	4.5	509	2	US-09-252-991A-24098	Sequence 24098, A
45	112.5	4.4	382	2	US-09-902-540-10508	Sequence 10508, A

ALIGNMENTS

RESULT 1									
US-10-033-109-14									
Sequence 14, Application US/10033109									
Patent No. 6833492									
GENERAL INFORMATION:									
APPLICANT: Allen, Stephen M.									
APPLICANT: Rafaleki, J. Antoni									
TITLE OF INVENTION: Nitrogen Transport Metabolism									
FILE REFERENCE: BB-1210									
CURRENT APPLICATION NUMBER: US/10/033,109									
CURRENT FILING DATE: 2001-12-28									
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625									
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27									
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248									
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998									
NUMBER OF SEQ ID NOS: 14									
SOFTWARE: Microsoft Office 97									
SEQ ID NO 14									
LENGTH: 470									
TYPE: PRT									
ORGANISM: Trilicium aestivum									
US-10-033-109-14									
Query Match 87.5%; Score 2216; DB 2; Length 470;									
Best Local Similarity 86.0%; Pred. No. 5.7e-213;									
Matches 404; Conservative 30; Mismatches 34; Indels 2; Gaps 1;									
QY	8	VPLAYQNTSASVADWLKNGDNAMQVLAATLVGLQSVPGILVVLVYGVVKKKMAVNSAFMA	67						
DB	3	VPLAYQNTSASVADWLKNGDNAMQVLAATLVGLQSVPGILVVLVYGVVKKKMAVNSAFMA	62						
QY	68	LVAFAAVICWTWAVNMSFGEKLLPIKWKARALDQGLVGRALPATVHYRADDSVET	127						
DB	63	LVAFAAVICWTWAVNMSFGEKLLPIKWKARALDQGLVGRALPATVHYRADDSVET	122						
QY	128	AAVEPYPMATVYVFCVFAITLLIVAGSLIGRMSFLAMVIVPVLMLFVSYVGAFLSW	187						
DB	123	AAVEPYPMATVYVFCVFAITLLIVAGSLIGRMSFLAMVIVPVLMLFVSYVGAFLSW	182						
QY	188	GGGFLFMWGVIDYCGGVVHVSAGIAGFTAAVYVGRPAQDRRPPNNILFTLTGAGLL	247						
DB	183	GGGFLFMWGVIDYCGGVVHVSAGIAGFTAAVYVGRPAQDRRPPNNILFTLTGAGLL	242						
QY	248	WMKAGFNGGGPYAANSVASMAVLTNITCTANSLIYWTCLDVFYFKKPSVGAVOGMITG	307						
DB	243	WMKAGFNGGGPYAANSVASMAVLTNITCTANSLIYWTCLDVFYFKKPSVGAVOGMITG	302						
QY	308	LVCITPAAGVVGWALVNGVLAGSLIPWYTMILHRSKILQVRDVLGVFHTHVGAGLL	367						

D_b 303 LVCITPGAGVVGGMALVWGVLGASVPWYTTMYVLHKKSKTLKQKVDPTLGVTHHGVAGILL 362

Q_y 368 GGLTGLFAEPFLCNFLFPVADSRGAFYGGAGAGCGKQIAGGLFVAAWNVVTSLICLA 427

D_b 363 GGVLGLFAEPFLCNFLFPVTSRGAIFYGNGAOLGKQIAGGLFVIGWNVVTSIIIVV 422

Q_y 428 INLTPFLRPDDKLEVGDDPAVHGESEAYALMGDEMDVTYKHGSDAIVAPV 477

D_b 423 IRLVPLPKMSSEKLAIGDDPAVHGESEAYALMGDEMDVTYKHG--AAVAPV 470

```

1      RESULT 2
2      US-10-033-109-12
3      Sequence 12, Application US/10033109
4      Patent No. 6833492
5      GENERAL INFORMATION:
6      APPLICANT: Allen, Stephen M.
7      APPLICANT: Rafalecki, J. Antoni
8      APPLICANT: Sakai, Hajime
9      TITLE OF INVENTION: Nitrogen Transport Metabolism
10     FILE REFERENCE: BB-1210
11     CURRENT APPLICATION NUMBER: US/10/033,109
12     PRIOR FILING DATE: 2001-12-28
13     PRIOR APPLICATION NUMBER: 09/384,625S
14     PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
15     PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,248
16     PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
17     NUMBER OF SEQ ID NOS: 14
18     SOFTWARE: Microsoft Office 97
19     SEQ ID NO 12
20     LENGTH: 486
21     TYPE: PRT
22     ORGANISM: Glycine max
23     US-10-033-109-12

```

Query Match	73.4%	Score 1860.5	-DB 2	Length 486
Best Local Similarity	71.9%	Pred: No. 2.2e-177		
Matches 341	Conservative 51	Mismatches 77	Indels 5	Gaps 2

QY	9	PLAYOGNTSASVADMLTKNDQNAOLVAATLVGLQSPGLVVLGVGVKKKMAVNSAFMAL	68
Db	4	PLAYOEHLPA - PMLTKNDQNAOLVAATLVGLQSPGLVVLGVGVKKKMAVNSAFMAL	62
QY	69	YAFAPAVICWTVTAYNMSFGKLLPTWGKARPALDGLLVGRALPATVHYRADGSVETA	128
Db	63	YAFAPAVLICWTVLCYMARFGEELFPWVGKAPALGQFLTKRAIVETIHHFNGVTESP	122
QY	129	AVEPLPYMAVTVYEOCVFAATILILVAGSLGMSFLAMMIAPVIMTFSTYTGAFSLWG	188
Db	123	PEBPYPMAVSLVYFOCTFAATILILVAGSLGMMNKAMAPVLMITFSTYTGAFSLWG	182
QY	189	GGFLFHMVGLDCCGVIVHVSAGIAGFTAAVYVGPRAQXDRERPPNNILFTLTGAGLW	248
Db	183	GGFLYQWGVIDYSGGVIHLSGIAAGFTAAVYVGPRLKSDREPPNNVLMLAGLW	242
QY	249	MGWAGPNGGCPYLAANSVASMAVINTMICTPMSLIVTCLDIVTFPKKPSVGAQVMITGL	308
Db	243	MGWMSGNGAPYAPAAVNTASIAVINTMICATSLVLTVDIVTFEFGKPSVGAQVMITGL	302
QY	309	VCITPAAGVVOGMAALVMGVLAGSIWYTMMLIHKKSKILQARDDTLGVNHTGAVAGLIG	368
Db	303	VCITPGAGLVQSMALVMGILSSIMVMTMLIHKSKSTLQAKDDTLGVNHTGAVAGLIG	362
QY	369	GLLTGLFAPBPTLCNLF.PVADSHGAFFYGGAGAQFGKQIAGLGFVUAMNVVTSLICLAT	428
Db	363	GLLTGLFAPBPTLCRLTLPTNNSGAFYGGGGVQFQKQIAPVAFVIGMNLVSTIIILVI	422
QY	429	NLLVFLRMDDLTLEVGDDPAVHGEAAALMDGEMVYDTGKS----DAAPV 478	
Db	423	KLFLPRMDEQLEIGDDAVHGEAAALWDDGKDYPTRGKS----QSGATVSPV 476	

```

, RESULT 3
, US-10-033-109-10
, Sequence 10, Application US/10033109
, Patent No. 6833492
, GENERAL INFORMATION:
, APPLICANT: Allen, Stephen M.
, APPLICANT: Ratajski, J. Antoni
, APPLICANT: Sakai, Hajime
, TITLE OF INVENTION: Nitrogen Transport Metabolism
, FILE REFERENCE: BB-1210
, CURRENT APPLICATION NUMBER: US/10/033,109
, PRIOR FILING DATE: 2001-12-28
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
, PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
, PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
, NUMBER OF SEQ ID NOS: 14
, SOFTWARE: Microsoft Office 97
, SEQ ID NO 10
, LENGTH: 497
, TYPE: PRT
, ORGANISM: Oryza sativa
, US-10-033-109-10

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Query Match	67.7%;	Score 1715.5;	DB 2;	Length 497;
Best Local Similarity	69.3%;	Pred. No. 7.4e-163;		
Matches 312;	Conservative 54;	Mismatches 83;	Indels 1;	Gaps 1.

[illegible]

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RESULT 4
US-09-252-991A-23745
; Sequence 23745, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

```


Query Match	25.3%	Score 641;	DB 2;	Length 439;
Best Local Similarity	33.6%	Pred. No. 2e-55;		
Matches 149;	Conservative	78;	Mismatches 167;	Indels 50;
Gaps 8;				
19	SVADWLNQGDNAWQVLAATLVGLQSGVPEGLVTVLYGSGVKKKNAVNSAFPAALVAFPAVWICW	78		

Query Match	25.2%	Score 639,	DB 2,	Length 433;
Best Local Similarity	33.7%	Pred. No. 3.2e-55;		
Matches 149;	Conservative 82;	Mismatches 159;	Indels 52;	Gaps 10;
QY	24	LNKGDNMALVLAATLVLGSLVPGVLVYVGGVKKKMAVSAFMAVYAFPAVMI	CVWTAAY	83
Db	31	IDKDNSSMLTCSALVFPFTTIPGIALFYGLLRKSNVLSLMTQMLTFSVII	ILIMNGY	90
QY	84	NMSF--GEKLLPIWGKARPALDOGLVGRALPATVHYRADGVSVEAAVEPL	YPMATVY	141
Db	91	SLAFTAGRK--IWG-----GMSLFEINNISVDVSAGE--INQYVHV		128
QY	142	FOCFPAATLTLVLVAGSLGGRMSFLAMMI FVPLMLTFESTVGAFAISLWG--G	GFLEPHGVTD	200
Db	129	FOGSPAVTVTALVGAIGERIRFASALLFTVIWTFESTIPIPAHWVGEGWL	IDDGALDF	188
QY	201	CGGVYIHVASAGIAFTAAVWGPBAOKDERFPENNITLFTLGAGLMMGAGFNG	GSGPY	260
Db	189	AGGVTVHINAVALVGAIVLLGKRGDYCHTAIKPHNLPMVFTGAVLVI	IGMFGFNAGSAG	248
QY	261	AANSVASAAVLTNTNICTMASLIVTCLDVIFFKKRPSVVGAVQGMITGLV	CTTPAAGVYG	320

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Db 249 SANGIALALFLNTVATAGAVLAWTFAEWLVRKXPSMLGSGSCGCIAGLVAITPAAGTGP 308
Qy 321 WAALVGVLAGSIPYTMMLHKRSKILORVDDTLGVFTHGVAGLGLTGLFAEPL 380
Db 309 IGALVIGIAGTIGMGVVLKRMWK---ADVDVDFGHGTGCIAGLGLTGIPT--- 360
Qy 381 CNLFLPVADSRAPFGAGGAGAO---FGKQIAGLGFVVA---MNVVTSICLAINLVP 433
Db 361 -----ASFAGGICYSCHMTLKGKQVLTQLPSVVTLLMSVVAIARADKLVG 409
Qy 434 LAMPDDKLEVG-DDAVHGEAY 454
Db 410 LRVSGEEHGDLDITTHGERAY 431

RESULT 7
US-09-328-352-5397
; Sequence 5397, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5397
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5397

Query Match 25.0%; Score 634.5; DB 2; Length 470;
Best Local Similarity 32.5%; Pred. No. 1e-54;
Matches 150; Conservative 82; Mismatches 176; Indels 53; Gaps 8;

Qy 3 SSATVPLVAYQNTSASVADMLNKGDNAQVLAATLVGLQSVPGIVLVYGVYKKKMAVN 62
Db 48 AITAAAPAEETPAATPTAKLDGTSTWILSTALVLTMTIPGLAFYGMVRKKXNVLS 107
Qy 63 SAFMALYAPAAVWICVNTVAVNMSPGEKLLPIWGKARPALDQGLVGRA--ALPATVHYR 120
Db 108 TMMPFSLAAILVSLMVAIGYGLAFSGT-----GAFGDLSKAMLVGAFDLSTGI--- 159
Qy 121 ADGSVETAAVEPLYPMATVTVYFCVPAATLLIVAGSLIGRMSFLAMMIFVPLMLTFEST 180
Db 160 -----PESLFIIFQMTFAITVAIILSGSIADRMKYSAFMAFIAMVLVVA 205
Qy 181 VGAFSLMG-GLFEMHGVLDYCGGYIHYSAIGAGTAAYWGPRAQKDBRPPNNILF 239
Db 206 PITHWVMAADGMLEFAGALDPAGTVHINSVAGLVAAVYMLGKRIGLCRSMAPNNIL 265
Qy 240 TLTGAGLLMMGNAFGGPPYANSVASNAVINTNICTAMSLIWTCLDVIFFKPSVVG 299
Db 266 TVIGASLLMVGMPFGVGSALGAGARASAILVTQVAAAAAASFMLVERMIRGKASVLG 325
Qy 300 AVQGMITGLVCTTPAAGVVGMAALVGVLAGSIPYTMMLHKRSKIIQVDDTLGVFH 359
Db 326 GASGAVAGLVITPAAGFVGAGALVGLIGVAVCFWGTAL---KRLIKDDALDAFG 381
Qy 360 THGVNAGLLGLTGLF-----AEPFLCNLFLPVADSRAPFGAGGAGNGQIAGL 411
Db 382 LHAVVGSIQAILTGVVYSDEITIAANAVALAPTF-----AGQLWVQVEGL 426
Qy 412 FVVAAMVVTSLICLAINLVLPRMPDKLEVG-DDAVHGE 451
Db 427 AMVYVSGIATPILKVIIDLIGRVNSDDERMGLDLSQGE 467

RESULT 8
US-09-134-001C-3907
; Sequence 3907, Application US/09134001C

; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3907
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3907

Query Match 23.0%; Score 582; DB 2; Length 437;
Best Local Similarity 29.7%; Pred. No. 1.6e-49;
Matches 136; Conservative 93; Mismatches 171; Indels 58; Gaps 11;

Qy 24 LNKGDNAQVLAATLVGLQSVPGIVLVYGVYKKKMAVNSAFMALYAPAAVWICVNTWAY 83
Db 22 MNMDITFLPCTILLVMT--PGLSLFYGLVQSKNMLNTWQSVVAIVTFVWIIIGF 80
Qy 84 NMSF-----GKTLPIWGKARPALDQGLVGRALPATVHYRAQSVETAVERLYP 135
Db 81 SLSPDGNQWIGLKF-----GL-----HH--VGFTSKTSLSPHP 115
Qy 136 MATVYFQCVPAATLLIVAGSLGRMSFLAMMIFVPLMLTFSTYGVAFSLMGGFPLHW 195
Db 116 LSLFPLQMFCTIAVSLSSIAEKRFIPLYLSLWVLIIISPAVHWVWGGWISKI 175
Qy 196 GVIDYCGYVIVHSAIGAGTAAVWVGPRAQKDBRPPNNILFTLTGAGLLMGWAGFN 255
Db 176 GAIIDVAGGTVAHITSGVGLVIGMIG--IGKKKEKHPHMLITLLIGILVLMGWYFN 233
Qy 256 GGGPFAANSVASMAVLTNICTAMSLIWTCLDVIFFKPSVGVAGVQGMITGLVCTPAA 315
Db 234 VGSATPFHIMISFVNVIAGSAGAFGMLIFEYILKKTSLGLGSLGSLVATPAA 293
Qy 316 GVVQGMALMVGVLGSIIPYTMMLHKRSKILORVDDTLGVFTHGVAGLGLTGLF 375
Db 294 GYVSTMSMTIITIGICCIYVINDI---KVKAQYNALDAFGHGGILGAVLTGVF 349
Qy 376 ----AEPFLCNLFLPVADSRAPFGAGGAGQFGKQIAGLGFVVAAMVVTSLICLAINL 431
Db 350 QSHQNSAVQNGFIYADPFKVVV-----QLGAIAIVVPSAIVTFELIARFIKF 399
Qy 432 VPLRMPDDKLEVGDA-VHGEBAVYLMGDGEMVDTYTKH 468
Db 400 TPLATTOBEDKYGDAIVHGEKAYFY---GELINKENRH 434

RESULT 9
US-09-902-540-15324
; Sequence 15324, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Steven C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15324
```



```

; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 398
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-398
Query Match 18.8%; Score 476; DB 2; Length 452;
Best Local Similarity 30.2%; Pred. No. 6.8e-39;
Matches 139; Conservative 70; Mismatches 180; Indels 72; Gaps 13;
```

```

QY 24 LKNGDNAMQLVATVGLQSVPGLVVLYGGVVKKKAIVASAFMAIYFAFAVIMCWTFWY 83
DB 1 MPPSLMIAWIAIPALYSLM-FPELSILYGMLOGCHVLTFFMMVMSLSGISVYIYGH 59
QY 84 NNSFEEKL-----LPIWGKARPALDOGLLVGRAALPATVHYRADSGSVETAVERPLY 134
DB 60 GLVLSIGSGWGIIGNPLEYFGFRNIMEDG-----TGDLMMAG----- 98
```

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QY 135 PMATVVYQCVFAATILLVAGSLIGRMSFLAMMIFVPLMTLFSYTGAF-----S 185
DB 99 -----FYILFAISLALVSAGAAGRMFGAMLVFGVLTFTFYAPLAHVFAIDDES 151
QY 186 LMGGGFL-----FHWGVIDYCGGYVIHVSAGIAGFTAAVYVGPRAQKDERFPNNILFT 240
DB 152 GYVGGMKGVLEFH-----DFAGGTAVHMMNAGASGLALAVIGRRHSM---AVRPHNLPLI 204
QY 241 LTGGLLMMGWAGNNGGFPYANSVASMAVLTNTICTAMSILVWTCUDVIFPKKPSVGA 300
DB 205 LIGAGLIVAGWFGFNGGTAGGANFLASTVVTSLAAAGSMGFMVLVERVFSKPTFGS 264
QY 301 VQGMITGLVCTTPAGVYQGWAAALVMGVLASIPWYTMILHKSILLQKVDDTLGVFHT 360
DB 265 ATGTAGIATTPAADAVSPIGAFVAGLGAIVGSFMA--ISMKG---HRVDDSPDVAV 319
QY 361 HGVAGLGLGLLTGLFAEPTLGNLPLVADSRGAFYGGAGAQFGKQIAGLFFVAMNVV 420
DB 320 HGMAGIAGALFVMLFGDP-----LAPAGVSGVFEGGELSLMBEPLA-IIVTLTYAFGV 372
QY 421 TSLICLAINLVPLRMPDD-KLEVDDAVHGEBAVALMGDG 460
DB 373 TWLIATILNKFTMLRTISEAEYEGIDRAEHAESAIVHLNSG 413
RESULT 12
US-09-487-558B-192
; Sequence 192, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.110
; CURRENT APPLICATION NUMBER: US/09/487,558B
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 192
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-192
Query Match 18.7%; Score 474.5; DB 2; Length 492;
Best Local Similarity 26.2%; Pred. No. 1.1e-38;
Matches 132; Conservative 87; Mismatches 205; Indels 79; Gaps 13;
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QY 4 SATVVPL---AYOGTASVADWLNKGDMAQVATVGLQSVPGLVVLYGGVVKKKA 60
DB 3 SRTTGPLTTEYDGTIV-----AFWIIIGALVLFPM-VFGLGFLVLSGLARRKSA 49
QY 61 VNSAFMAIYFAFAVIMCWTFWYNNNSFGEKLLPIWGKARPALDOGLLVGRAALPATVHYR 120
DB 50 LALIIVVLMATLVGLQVYFPGYSIAF-----SKSAP-----NNK 84
QY 121 ADGSVETAAV-----EPLYPMATVYVYQCVFAATILLVAGSLIGRMSFLAMMIFV 171
DB 85 FIGNLDSFGFRNVYGGKPEDADAYPELAYATFOQMFSCVNLISIAGTAEGRRLLPHWVFL 144
```

QY 172 PLMLTSTYVGAFLWG--GGFLFMGVIDYCGGVIVHSAGINGFTAAVWGPRAQDR 230
DB 145 FIATITGCPVTVTWISPGMAVOWGLWAGGNIELISAVGFYVWFLGRNEKLI 204
QY 231 REPNNILFLTAGLLMGMAGFNGGPPAANSVASMALVNTNICTAMSLIWTCLDVI 290
DB 205 NRPENHVSIVLTGSLTLMFGMLFPNSASSLPULRSYAFAMTCLSAITGCMWCLDR 264
QY 291 FPKPSVGAQVGMITGLVCTPAGVGVGMALVNGVLGSIIPWYTMILHRSKILOR 350
DB 265 SEKKMSTVGLCSGIIISGLVATPSSGICITLYSLIGIVAGVCMFATKL-----KYAK 319
QY 351 VDDTLGVPHFTHGAGLLGLLTGLPAEPTLCNLFPLVDSRGAPYGG---AGAGRGKOI 407
DB 320 VDDAMPILAEHGVAGVIGLIFNALFGADVIGM-----DGTTEHEGWTNHYKQYKOI 374
QY 408 AGGLFVAVMNVVTSICLAINLLVPLR-----MPDDKL-EVGDDAVHGEAAYA 455
DB 375 AYTAASIGTAAVTAIICFVLGIIIPGMRLISEAEAGHDEIQIGFAVDYVEVRDYY 434
QY 456 LMG---DGEWYDVKHGSAAVA 475
DB 435 LMGVDEDSQSRSDVNHRYNNAHLA 457

RESULT 13
US-08-635-967-2
; Sequence 2, Application US/08635967
; Patent No. 6620610
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Bernd
; APPLICANT: NINNEMAN, Olaf
; TITLE OF INVENTION: DNA SEQUENCES FOR AMMONIUM TRANSPORTER,
; TITLE OF INVENTION: PLASMIDS, BACTERIA, YEASTS, PLANT CELLS AND PLANTS
; TITLE OF INVENTION: CONTAINING THE TRANSPORTER
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostroienk, Faber, Gerb & Soffen, LLP
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,967
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP 94/03499
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 37 597.9
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weilmann, Edward
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-635-967-2
Query Match 13.4%; Score 338.5; DB 2; Length 501;
Best Local Similarity 25.7%; Pred. No. 4,5e-25;
Matches 134; Conservative 64; Mismatches 220; Indels 103; Gaps 18;
QY 1 MSSATVPLVAYQNTSAS-----VADMLKNG-----DNAMQVATVAGLSVPG 46
DB 1 MCSATIDLVLLGAPNATAAANYICGQLGDNVKNKFTDPAIDNTYLLFSAIVLFSQNL-G 59
QY 47 LVLYGCVVKKKMAVNSAFMALYAPAAVVICWYTAAYNSFSEKLLPIWGKAPALDQGL 106
DB 60 FAMLGAGSVRAKNTVMIMLTNVLDAAGLFYLLFGYAPAFSPNSNGFKG----- 110
QY 107 LVGRALPATVHYRADGSVETAAVEPLVPMATVVVYFQCFAATLILVAGSLGRMSFLA 166
DB 111 -----HYFGIKDIPITASD-----YSNFLYQMFAIAAGITSGSIARTQFYA 154
QY 167 WMIFVPLMLTFSTYVGAFLWG-----GGFLFMGVIDYCGGVIVHSAGIAGF 215
DB 155 YLIISSFLTGFTYPPVYSHFMSVYDGWASPFRIDGDLFSTGALDPAQSGVHMVGSIAGL 214
QY 216 TAAVWGPRAQDRERFPNNILFTLTGAG-----LWMGMAGFNGG----- 257
DB 215 WGLALIEGPRL---GRFDNGRAIALRGHSASLVLDGTFLLWFGWYGFNPGSFNKILVTV 270
QY 258 --GPYAA--NSVASNAVLTNICTAMSLIWTCLDVIFFPKP-----SVGAVQGMITG 307
DB 271 ETGTVNGQMSAVGRTVITTLTAGCTA-----ALTTLEGKLLSGHMVTVVCGNLGG 323
QY 308 IVCITPAGVGVGMALVNGVLGSIIPWYTMILHRSKILORV--DPTLGVFHTHGVAG 365
DB 324 FAITGGCSVEPMALITGFAVA-----LVLAGCNLAERKTKDPLEAAQLHGCGG 376
QY 366 ILGSLITGLFAEPTLCNLFPLVADSR--GAFYGAAGAGFOGQIAGLFPVAMNVVTSI 423
DB 377 AMGLITFALFAQEKYINQYGNKPGPHGLFMNG--GKLLGALQLIIVITGVASATMGT 435
QY 424 ICLAINLLVPLRM-PDDKLEVGDDAVHGEAAYALMGDGMV 463
DB 436 LFFILKKMKLIRIISSEDEMAQMDMTRHGGFAVYFPDDESH 476

RESULT 14
US-09-134-000C-5907
; Sequence 5907, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5907
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-5907

Query Match 13.2%; Score 335; DB 2; Length 361;
Best Local Similarity 24.9%; Pred. No. 6.4e-25;
Matches 98; Conservative 69; Mismatches 155; Indels 72; Gaps 10;
QY 46 GLVLYGVVKKKKMAVNSAFMALYAPAAVVICWYTAAYNSFGEKLLPIWGKAPALDQGL 105
DB 24 GVLYLVVGLVNHRYIHHTLILGLVTLISGTLCLMLFVGYSLSF-----FGN----- 68
QY 106 LLVGRALPATVHYRADGSVETAAVEPLVPMATVVVYFQCFAATLILVAGSLGRMSFL 165

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2006, 19:25:14 ; Search time 20323 Seconds
(without alignments)
11569.880 Million cell updates/sec

Title: US-10-713-648a-29

Perfect score: 3677
Sequence: 1 aaataaaaacataagta.....aagctccatatttccaaaa 3677

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 6366136 segs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
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12: gb_hcg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2541.6	69.1	110000	4	AP008209_350
2	2541.6	69.1	171376	4	AC104487
3	746.4	20.3	1790	4	AK100411
4	733.6	20.0	1441	4	AK069311
5	529.2	14.4	1656	2	AR628380
6	529.2	14.4	1656	2	BT009273
7	528.2	14.4	1521	4	AY428038
8	454	12.3	1577	4	AB083582
9	454	12.3	4067	4	AK120352
10	454	12.3	110000	4	AP008207_377
11	454	12.3	148892	4	AP003235
12	392.6	10.7	5153	4	AB083581
13	392.6	10.7	110000	4	AP008207_355
14	392.6	10.7	110000	4	AP008211_228
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16	392.6	10.7	143515	4	AP003252
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18	389.2	10.6	1883	2	AR628378

19	388	10.6	1957	4	AK065288
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22	385.4	10.5	1717	4	AK102106
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24	375.6	10.2	137046	4	AP004775
25	372.6	10.1	1870	4	AK108711
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ALIGNMENTS

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Query Match

Best Local Similarity

Matches 3260; Conservative

69.1%; 85.2%; 0;

Score 2541.6; Pred. No. 0;

DB 4; Length 110000;

Mismatches 219; Indels 347; Gaps 24;

QY	166	CAAGCGAGTCAAAATGGTTAATCGATCGCACCTGACCATGATCCTCTATAT----	221
DB	24348	CTAAGGAGTCAAAATGGTTAATCGATCGCACCTGACCATGATCCTCTATATCCT	2440
QY	222	---AAGTCCCTCTAACTAGCTGACTGATACCAAAAG--GCATACAACTT	275
DB	24408	ATATAGCTGCTCTAACTAACTAACTAGATACCAATTTAAAGAACATACCTAAGCTT	2446
QY	276	AGTGTGTGTTAAATACGCGAGGAAGATGTGTCGTCCGCGCGAGCGGTGGCCGCTGGGCTA	335
DB	24468	AGTGTGTGTTAAATACGCGAGGAAGATGTGTCGTCCGCGCGAGGTGGCCGCTGGGCTA	2452
QY	336	CCAGGGGACAACGTCGCGCGTCCGTGCGAGCTGGCTGAACAAGGGGGACAACGCGTGGCA	395
DB	24528	CCAGGGGACAACGTCGCGCGTCCGTGCGAGCTGGCTGAACAAGGGGGACAACGCGTGGCA	2458
QY	396	GCTGTGTGCGCGCGACGCTGTGGGGCTGCAAGCGGTGCGGGCTTGTGTGCTGTACGG	455
DB	24588	GCTGTGTGCGCGCGACGCTGTGGGGCTGCAAGCGGTGCGGGCTTGTGTGCTGTACGG	2464
QY	456	CGGGGTGTGTAAGAAAGATGTGGGGCGGTGAATCGCGCTTCAATGGCGCTTACGCGCTTCG	515
DB	24648	CGGGGTGTGTAAGAAAGATGTGGGGCGGTGAATCGCGCTTCAATGGCGCTTACGCGCTTCG	2470
QY	516	CGCGGTGTGATCTGTGCTGGGTCAACCTGGGGCTTACAACATGTCTGTTCGGGGAGAACTCT	575
DB	24708	CGCGGTGTGATCTGTGCTGGGTCAACCTGGGGCTTACAACATGTCTGTTCGGGGAGAACTCT	2476
QY	576	CCCGATCTGGGGGAAAGCGCGCGCGCGCTGGAACCAAGGGCTCTCTGTGTGCGCGCGCG	635
DB	24768	CCCGATCTGGGGGAAAGCGCGCGCGCGCGCTGGAACCAAGGGCTCTCTGTGTGCGCGCGCG	2482
QY	636	GCTGTGCGGCGACGCTTCCATCACTACCGCGCGGACGCGTGGAGAACGGGGCGGTGGAGCC	695
DB	24828	GCTGTGCGGCGACGCTTCCATCACTACCGCGCGGACGCGTGGAGAACGGGGCGGTGGAGCC	2488
QY	696	GCTGTAAACCAATGGAGGACGATGTGTGATCTTCAAGTGCATGTTTCGCGCGCATCACCTTCAT	755
DB	24888	GCTGTAAACCAATGGAGGACGATGTGTGATCTTCAAGTGCATGTTTCGCGCGCATCACCTTCAT	2494
QY	756	CCTGTGTGCGCGGCTCCCTCTTCGCGCGCGCATGACTTCTTCGCTTGATGATCTTTCGTC	815
DB	24948	CCTGTGTGCGCGGCTCCCTCTTCGCGCGCGCATGACTTCTTCGCTTGATGATCTTTCGTC	2500
QY	816	GCTGTGAGCTCACCTTCTCTTACACCGTGTGGGCTTCTTCCTCTTGGGGCGGCGCTTCT	875
DB	25008	GCTGTGAGCTCACCTTCTCTTACACCGTGTGGGCTTCTTCCTCTTGGGGCGGCGCTTCT	2506
QY	876	CTTCCACTGGGGCGCATCGACTATGCGGGGGGCTACGTCAACAGCTTCGCGCGGAT	935
DB	25068	CTTCCACTGGGGCGCATCGACTATGCGGGGGGCTACGTCAACAGCTTCGCGCGGAT	2512
QY	936	CGCGGCGCTTACCGCGCGCTTACGTGCTCCGTAACAAGCCTCATCTTTTGTCTATACT	995

Db	25128	CGCGGGCTTACACCGCCGCTACTAGGGTCGTACACACAGTCTCATCTTTGCTTAAGCT	2518
Qy	996	TATATCTGATGAGCCAGTATTTAAATTTTCAATC---ATAAATTTAAAGCTAAATTTTGA	1051
Db	25188	TATATCTATAGCCAAATATTTAAATTTTAACTTATATTAATTTAAAGCTGATTTTGA	2524
Qy	1052	GTTTTTTTCAATCGAAGTTTATTTTTTCAATTTGTTTTTAAAGTCGTAAACAACGTATA	1111
Db	25248	G-CTTTTTCAATCGAAGTTTATTTTTTCAAGCCTT---TTTTAAGTTGCTTAAGAAACATATATA	2530
Qy	1112	TAAAGTTTTATTCACAAATTAATCTATATCTTCAAGACTAAGCTAAACAATAGTACTCAC	1171
Db	25305	TAAAGTTTTATTCACAAATTAATCTATATCTTCAAGACTAAGCTTAACAATAGTACT----	2536
Qy	1172	TTTTGCCGCGCGCGACGTCGACGTAGTCTTGACAAGTGTAC---ATAATCAATGTGT	1227
Db	25361	-----CCGCGCGCGCGACGTCGAAAGTGGTCTTGACAAGTGTACATATATATCAATGTGT	2541
Qy	1228	GGCTGGCAAGTGGGGGCCAAGGGCGCAGAAAGACAGGAGAGGTTCCCGCCGAAACAATATA	1287
Db	25416	GGCTGGCAAGTGGGGGCCAAGGGCGCAGAAAGACAGGAGAGGTTCCCGCCGAAACAATATA	2547
Qy	1288	CTGTTTCAAGCTGACAGGGGGGAGGGCTGTGTGATGGGGTGGGAGGGGTTCAACGGCGCG	1347
Db	25476	CTGTTTCAAGCTGACAGGGGGGAGGGTTTCTATGTATGGGGTGGGAGGGGTTCAACGGCGGT	2553
Qy	1348	GGTCCGTACGCGCGCAACCTCGGTGCTCTTATGGCCGTCTCTCAACACACATCTGCAAC	1407
Db	25536	GGTCCGTACGCGCGCAACCTCGGTGCTCTTATGGCCGTCTCTCAACACACATCTGCAAC	2559
Qy	1408	GCCATGAGCCTCATGCTGTGTGACATGCTCTGAGTCACTTTCTTCAAGAAAGCCTCCGTCT	1467
Db	25596	GCCATGAGCCTCATGCTGTGTGACATGCTCTGAGTCACTTTCTTCAAGAAAGCCTCCGTCT	2565
Qy	1468	GTGGGCGCCGCTCCAGGGGCAATGATCACCGGCTGTGTTGATCATACCCCGCTGAGATGAC	1527
Db	25656	GTGGGCGCCGCTCCAGGGGCAATGATCACCGGCTGTGTTGATCATACCCCGCTGAGATGAC	2571
Qy	1528	TAAATCATCACTACACGAAAAAGAAAGCCTTATTAATTAAGTATTAAGCTTAAATTAAT	1587
Db	25716	TCAATTCATCACTACACGAAAAAGAAAGCCTTATTAATTAAGTATTAAGCTTAAATTAAT	2577
Qy	1588	TAAAGTAAATTAATGTGATTAATTTTTT-----CTTAGAAAAATTTCTGCG	1631
Db	25776	TAAAGTAAATTAATGTGATTAATTTTTTAAAAAAACAATCTTGTATCAAAACCTTTTACG	2583
Qy	1632	AAAAATATACATTTAGTATTTTGGCAATA---GTGTGTAGAAAAAGAAAGTGTGAAGTT	1688
Db	25836	AAAAATATACATTTAGTATTTTGGGAAAGACACGTATGCAAAAAAGAAAGGTTGAAGTT	2589
Qy	1689	GAAAAAATGAGTACCGAACACACAGCCTTATTAATTAATCAAAATTTGTGTAGTACTTAAT	1748
Db	25896	GAAAAAATGAGTACCGAACACACAGCCTTATTAATTAATTAATTTGTGTAGTACTTAAT	2595
Qy	1749	TAACTTTGGATGATGAACTATTAACGTATGCGCGCGGTGACGAGCGCGATGCAATCT	1808
Db	25956	TAACTTTGGATGATGAACTATTAACGTATGCGCGCGGTGACGAGCGCGATGCAATCT	2601
Qy	1809	TAAATTAAGTATGATTAATCCCGGTTTGGAGATTAATATCTTCCCGCCAGAGTTGTTTTG	1868
Db	26016	TAAATTAAGTATGATTAATCCCGGTTTGGAGATTAATATCTTCCCGCCAGAGTTGTTTTG	2607
Qy	1869	ACTTTGAATCTAAACGTCTGCGGTTTGCACAAATACAGGAGGTTGGTTTACTTGTGCTGC	1928
Db	26076	ACTTTGAATCTAAACGTCTGCGGTTTGCACAAATACAGGAGGTTGGTTTACTTGTGCTGC	2613
Qy	1929	CAAAATATCTGCATTTTCCCGGTATGATTAAGCGCGTTTATACCATTTTGTGGCACTAATTA	1988
Db	26136	CAAAATATCTGCATTTTCCCGGTATGATTAAGCGCGTTTATACCATTTTGTGGCACTAATTA	2619
Qy	1989	GCACGACAGCACTGATTCATCA---TATCTCTTCTCACTCTCTTGTATGTGAGAGA	2044

[illegible]

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QY	2975	GATCTTCAGGCGGTGACGACACACCTCGGCGTCTTCCACACCCAGCGGTGCGCGCT	3034
Db	27439	GATCTTCAGGCGGTGACGACACACCTCGGCGTCTTCCACACCCAGCGGTGCGCGCT	27498
QY	3035	CTTGGGGGCGCTCTCTCAACGGGCGCTTTGGCGAGGCCACCGCTGCAACCTGTCCTGCC	3094
Db	27499	CTTGGGGGCGCTCTCTCAACGGGCGCTTTGGCGAGGCCACCGCTGCAACCTGTCCTGCC	27558
QY	3095	CGTGCAGCACTCCCGGGGCGCTTCTTACAGCGGCGCGCGCGCGCCAGTTGGGCAAGA	3154
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QY	3155	GATGCGCGGCGGCTCTTTCGTGCTCGGCTTGGAACTGTGTGTATCACTCCCTCATCTGGCT	3214
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QY	3215	CGCCATCAACCTCTCGTCCGCGTCCGATGCGCCGACGACAAAGCTCGAGGTGCGCGACGA	3274
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DEFINITION	Oryza sativa chromosome 3 BAC OSUNBA0042109 genomic sequence,				
ACCESSION	AC104487				
VERSION	AC104487.3	GI:28269486			
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SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
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AUTHORS	1 (bases 1 to 171376) Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M.,				

TITLE	Overton D.L., Teltin,T., Kim,M.M., Bera,J.V., Jin,S.S., Patoch II,W., Tallon L.J., Koo,H., Zisman,V., Hsiang,J., Blunt,Yanaken,S.S., Riedmiller,S.B., Uteback,T.T., Feldblum,T.V., Yang,Q.Q., Haas,B.V., Suh,B.B., Peterson,J.J., Quackenbush,J., White,O., Salzberg,S.L. and Fraser,C.M.
JOURNAL	Oryza sativa chromosome 3 BAC OSUNBa0042109 genomic sequence Unpublished
REFERENCE	2 (bases 1 to 171376)
AUTHORS	Buell,R.
JOURNAL	Direct Submission Submitted (12-DEC-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
REFERENCE	3 (bases 1 to 171376)
AUTHORS	Buell,R.
JOURNAL	Direct Submission Submitted (07-FEB-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
REFERENCE	4 (bases 1 to 171376)
AUTHORS	Buell,R.
JOURNAL	Direct Submission Submitted (14-FEB-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
REFERENCE	5 (bases 1 to 171376)
AUTHORS	Buell,R.
JOURNAL	Direct Submission Submitted (15-FEB-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
COMMENT	On Feb 7, 2003 this sequence version replaced gi:18497084. Address all correspondence to:rice@tigr.org

BAC clone OSUNBa0042109 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC clone.

Genes were identified by a combination of several methods: Gene prediction programs including Egenes (<http://www.softberry.com/>), genescan and Genescan+ (Chris Burge, <http://CCK-081.mtc.edu/GENSCAN.html>), GeneMarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/GeneMark/>), and Gensplice (Mhaela Perrea and Steven Salzberg, contact_mperrea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/cdb/cgi.shtml>)

Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/repeatmasker.html>). This BAC overlaps with rice BAC OSUNBa0096106 (AC092557) and OSUNBa0075M12 (AC096856).

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Db	77517	TTTGTAGTTGTTAAATAGTACCTAGTTGTTGATCTTACTGATGATGAAAC	77458
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RESULT 3			
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LOCUS		1790 bp	mRNA
DEFINITION		Oryza sativa (japonica cultivar-group)	linear
ACCESSION		AK100411	PLN 24-JUL-2003
VERSION		AK100411.1	GI:32985620
KEYWORDS		FLI CDNA; CAP trapper.	
SOURCE		Oryza sativa (japonica cultivar-group)	
ORGANISM		Oryza sativa (japonica cultivar-group)	
REFERENCE			
AUTHORS			
1		The Rice Full-length cDNA Consortium, National Institute of	
2		Agrobiological Sciences Rice Full-length cDNA Project Team;	
3		Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,	
4		Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,	
5		Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,	
6		Ohneda, E., Shishiki, T., Foundation of Advancement of International	
7		Science Genome Sequencing & Analysis Group; Otsu, Y., Murakami, K.,	
8		Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,	
9		Kurosaki, T., Kodama, T., Maeda, H., Kobayashi, M., Xie, Q., Lu, M.,	
10		Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikiura, J.,	
11		Ikedo, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J.,	
12		Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;	
13		Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,	
14		Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,	
15		Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Otsu, N., Ota, Y.,	
16		Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,	
17		Yoshino, M., and Hayashizaki, Y.	
18		Collection, mapping, and annotation of over 28,000 cDNA clones from	
19		japonica rice	
JOURNAL		Science 301 (5631), 376-379 (2003)	
PUBMED		12869764	
REFERENCES			
AUTHORS			
1		(bases 1 to 1790)	
2		Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,	
3		Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,	
4		Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,	
5		Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,	
6		Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,	
7		Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,	
8		Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,	
9		Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,	
10		Maeda, H., Matsubara, K., Matsuyama, T., Mura, J., Miyazaki, A.,	
11		Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,	
12		Namiki, T., Narikawa, R., Nikiura, J., Nishi, K., Nomura, K.,	
13		Numesaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,	
14		Otsu, N., Ota, Y., Otsu, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,	
15		Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,	
16		Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,	
17		Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, F.,	
18		Tagawa, A., Takahashi, F., Takaku-Akahita, S., Tanaka, T., Tomaru, A.,	
19		Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,	
20		Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and	
21		Yoshimura, A.	
JOURNAL		Direct Submission	
1		Submitted (27-AUG-2002) Shoeni Kikuchi, National Institute of	
2		Agrobiological Sciences, Department of Molecular Genetics, Head of	
3		Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki	
4		305-8602, Japan [E-mail:skikuchi@ias.affrc.go.jp,	

COMMENT			
1		Tel:81-29-838-7007, Fax:81-29-838-7007)	
2		This clone is one of the 28K full-length cDNA clones from japonica	
3		rice.	
4		URL : http://cdna01.dna.affrc.go.jp/cDNA/NIMS	
5		NIMS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,	
6		Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,	
7		Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,	
8		Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and	
9		Yamamoto, M.	
10		PAIS Genome Sequencing & Analysis Group; Otsu, Y., Iida, Y.,	
11		Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,	
12		Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Maeda, H., Mura, J.,	
13		Mizuno, K., Narikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S.,	
14		Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,	
15		Yoshimura, A., Matsubara, K., and Murakami, K.	
16		Genome Exploration Research Group in Riken Genomic Sciences Center	
17		and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,	
18		Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,	
19		Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,	
20		Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,	
21		Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,	
22		Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,	
23		Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,	
24		Nakamura, M., Nishi, K., Nomura, K., Numesaki, R., Ohno, M., Otsu, N.,	
25		Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,	
26		Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,	
27		Sogabe, Y., Tagami, M., Tagami-Takeda, F., Tagawa, A., Takahashi, F.,	
28		Takaku-Akahita, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,	
29		Yasunishi, A., and Hayashizaki, Y.	
FEATURES			
1		Location/Qualifiers	
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3		/organism="Oryza sativa (japonica cultivar-group)"	
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5		/db_xref="taxon:39947"	
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4		Matches 780; Conservative	0; Mismatches 11; Indels 7; Gaps 2;
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Qy	2939	GTGTATACCATGATGATCTCTCCACAGCGCTCCCAAGATCTCTGACGCGCTGCAGCAC	2998
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Qy	2999	CCTCGGCGCTCTCCACACCGGCGGCGGCTCTCGGCGGCGCTCTCCACCGGCT	3058
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Qy	3059	CTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT	3118
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Qy	3179	CGGCTGGAACGTCGTCACCTCCCTATGCTCTCCGCAACCTCTCTGCTGCTGCT	3238
Db	1296	CGGCTGGAACGTCGTCACCTCCCTATGCTCTCCGCAACCTCTCTGCTGCTGCT	1355
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 Db 1652 GCACCTTTCAGATTCACAGGAGTCGGCTTCTGATTTTGTATGTTGTAATAATGATTA 1711
 QY 3596 CGTAGTTTGTATCTTACTGATGATGATGAACACAGATGATATATATATTTGTTAA 3655
 Db 1712 CGTAGTTTGTATCTTACTGATGATGATGAACACAGATGATATATATTTGTTAA 1771
 QY 3656 TTAAGCTCCATATTTTCC 3673
 Db 1772 TTAAGCTCCATTTTCC 1789
 RESULT 4
 AK069311
 LOCUS
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023012M17, full insert sequence.
 ACCESSION AK069311 GI:32979335
 VERSION AK069311.1
 KEYWORDS FLI CDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1
 AUTHORS The Rice Full-length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length CDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 TITLE Collection, mapping, and annotation of over 28,000 CDNA clones from japonica rice
 JOURNAL Science 301 (5631), 376-379 (2003)
 PUBMED 12869764
 REFERENCE 2 (bases 1 to 1441)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashidume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kobayashi, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,

Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, H., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sasaki, D., Sano, H., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
 Direct Submission
 Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-1 Kamponda, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
 This clone is one of the 28k full-length cDNA clones from japonica rice.
 URL: http://cdna01.dna.affrc.go.jp/cDNA/
 NIAS Rice Full-length CDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.
 FALS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
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ORIGIN

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Db 1440 TT 1441

RESULT 5
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DEFINITION Sequence 13 from patent US 6833492.
ACCESSION AR628380
VERSION AR628380.1 GI:59751057
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1656)
AUTHORS Allen,S.M., Rafalski,J.A. and Sakai,H.
TITLE Nitrogen transport metabolism
JOURNAL Patent: US 6833492-A 13 21-DEC-2004;
E. I. du Pont de Nemours and Company; Wilmington, DE
FEATURES
source 1.1656
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Best Local Similarity 86.9%; Pred. No. 1.5e-105;
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QY 426 GAGCGTCCGCGGCTTGT 485
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QY 546 GTACAACATGTCTGT 605
| | | | |
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| | | | |
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| | | | |
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| | | | |
Db 443 CGGCAAGCTGTGAAGAGCGCGCGGT 502
| | | | |
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| | | | |
Db 503 CCAGTGCATGTCTGT 562
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Db 563 GAGCTTCTCTGT 622
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Db 623 GCGCTTCTCTGT 682
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QY 906 CGGCTACGTCATCAAGTCTCGCGCGGATCGCGGCTTTCACCGCGGCTTACTGGGTCG 965
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Db 683 CGGCTACGTCATCAAGTCTCGCGCGGATCGCGGCTTTCACCGCGGCTTACTGGGTCG 742
| | | | |
QY 966 TACTAACAGC 975
| | |
Db 743 GCCAAGGACC 752

RESULT 6
BT009273
LOCUS BT009273 1656 bp mRNA linear PLN 20-JUN-2003
DEFINITION Triticum aestivum clone wlk8.pK0013.b6:fls, full insert mRNA
sequence.
ACCESSION BT009273
VERSION BT009273.1 GI:32128824
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE 1 (bases 1 to 1656)
AUTHORS Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
FEATURES
source 1.1656
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wIk8.pK0013.b6:fls"

Query Match 14.4%; Score 529.2; DB 4; Length 1656;
Best Local Similarity 86.9%; Pred. No. 1.5e-105;
Matches 582; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy		306	GTGCTCGGCGCA	CGGTGGTGGCCGCTGGCTGACACAGGGGAAACA	GTGCGGTGGTGGCGGA	365
Db		83	GTTCGGGCAAGATGTCGGTGGCCGGTGGCCTACACAGGGGAAACA	GTGCGGTGGTGGCGGA	142	
Qy		366	CTGGCTGAACA	CAAGGGGGGACAACAGCGTGGCACTGGTGGCGGCGACTGATGGGCTTGCA	425	
Db		143	CTGGCTGAACA	AGGGGCCACAACAGCGTGGCACTGACGGCGGTCCACGCTGTGTGGGCTCAT	202	
Qy		426	GAGCGTCGGGGCTTGGTGGTGGCTGTACCGCGCGGCGCTGGTGAAGAAAGTGGGCGGTGA	485		
Db		203	GAGCGTCGGGGCAATGGTGGTGGCTGTACGGCGGGCGCTGTGAAGAAAGTGGGCGGTGA	262		
Qy		486	CTGGGCGGTTCATGGGGGCTCTACGGCTTCGCGCGGTGGATCTGCTGGGTCACTGGGCG	545		
Db		263	CTTCGGCTTCATGGGGGCTCTACGGCTTCGCGCGGTGTGAATCTGCTGGGTGTGGGCG	322		
Qy		546	GTACAAATGTCGTTTCGGGGAGAACTTCGCCGATCTGGGGGAAAGCGCGGCGCGCT	605		
Db		323	CTACAAATGTCCTTCGGCGAGAGCTGCTCCGTTCTGGGGCAAGCGCGGCGCGCT	382		
Qy		606	GGACCAAGGGCTCTCGTGGGCGCGCGCGCTGCGGCGAGCGTCCACTACCGGCGCGA	665		
Db		383	CGACCAAGGCTCTCTCGTGGGCGCGCGCTCGCTCCGCGCAACCGGCACTACCGGCGAGA	442		
Qy		666	CGGCAAGCGTGGAGACGGGGGGGGTGGAGACCGCTGACCCGATGGGAGAGGTGTACTT	725		
Db		443	CGGCAAGCTCGAGACGGGCGATGTGGAGCCCTACTTCCCATGGCCACCGGTGTACTT	502		
Qy		726	CCAGTGGCGTGTGGCGCGCATCACCCCTGATCTCGTGGCGGCTTCCTCGGCGCGAT	785		
Db		503	CCAATGGGTGTTCGGCGGCGCATGACGCTCATCTGGTGGCCGGGTGCGTGTGGGCGCAT	562		
Qy		786	GAGCTCTCTCGCCTGGATGATCTTGTGTCCGCTCTGGGCTCACCTTCTCTTACACCGTGG	845		
Db		563	GAGCTCTCTGGCGTGGATGCTTTCGTGTCGCGCTGGGCTCACCTTCTCTTACACCGTGG	622		
Qy		846	CGCCTTCCTCCCTCGGGGGCGGGGCGCTTCCTCTTCACCTGGGGCGCATCGACTACGGCG	905		
Db		623	CGCCTTCCTCCGTTGGGGCGGGGCGCTTCCTCTTCACCTGGGGCGCATCGACTACGGCG	682		
Qy		906	CGGCTACGTCATCCACGTCCTCGCGCGGCGATCGCGCGGCTTCAACCGCGGTTTACTGGGTCCG	965		
Db		683	CGGCTACGTCATCCACATCCCGCGGGGTGGCGGCTTCAACCGCGGTTACTGGGTCCG	742		
Qy		966	TACTTAACAGC	975		
Db		743	GCCAAAGAC	752		
RESULT 7						
LOCUS	AY428038	1521 bp	mRNA	linear	PIN 01-MAR-2004	
LOCUS	AY428038		Triticum aestivum ammonium transporter AMT2.1 (Amt2.1) mRNA,			
ACCESSION	AY428038		complete cds.			
VERSION	AY428038.1	GI:40548579				
KEYWORDS						
SOURCE						
ORGANISM						
			Triticum aestivum (bread wheat)			
			Triticum aestivum			
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP			
			clade; Poideae; Triticeae; Triticum.			
REFERENCE						
AUTHORS			Zhao,X., Yang,G., Tong,Y., Li,B., Miao,J. and Li,Z.			
TITLE			Isolation and expression analysis of an ammonium transporter,			
JOURNAL			Taamt2.1, from Triticum aestivum			
REFERENCE			2. (bases 1 to 1521)			
AUTHORS			Zhao,X., Yang,G., Tong,Y., Li,B., Miao,J. and Li,Z.			
TITLE			Direct Submission			
JOURNAL			Submitted (04-OCT-2003) The State Key Laboratory of Plant Cell and			
			Chromosome Engineering, Institute of Genetics and Developmental			

FEATURES		source	
Biology, The Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, China			
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ORIGIN			
Query Match	14.4%;	Score 528.2;	DB 4; Length 1521;
Best Local Similarity	87.4%;	Pred. No. 2.5e-105;	
Matches 578;	Conservative 0;	Mismatches 83;	Indels 0; Gaps 0;
QY	315	GACGATGTCGCGCTGGTGCATCAAGGGGAAACAGTCGCGTGCCTGCGACTGCA	374
DB	23	GATGTCGATGTCGCGGTCACAGGGGAAACAGTCGCGCGCTGCGCTGCA	82
QY	375	CAAGGGGAAACAGCTGTCGACGTCGTGCGCGGACGCTGTCGGGCTGCAAGCGTCC	434
DB	83	CAAGGGGAAACAGCTGTCGACGTCGTGCGCGCTGCAAGCGTGCCTCATGAGGTGCC	142
QY	435	GGGCTGGTGTGCTGTACGCGCGCGCTGTGTAAGAAAGATGGGCGGTGAACCTCGCGCTT	494
DB	143	GGGCTGGTGTGCTGTACGCGCGCGCTGTGTAAGAAAGATGGGCGGTGAACCTCGCGCTT	202
QY	495	CATGGCGCTACAGCGCTTTCGCGCGCGCTGTGATCTGCTGGGTCACTTGGGCGTACACAT	554
DB	203	CATGGCGCTACAGCGCTTTCGCGCGCGCTGTGATCTGCTGGGTCACTTGGGCGTACACAT	262
QY	555	GTCTGTGGGGAAGAGCTCTTCCTCGGATTTGGGGGAAGGCGCGCGCTGTCGACCAAGG	614
DB	263	GTCTGTGGGGAAGAGCTCTTCCTCGGATTTGGGGGAAGGCGCGCGCTGTCGACCAAGG	322
QY	615	CCTCTGTGTCGCGCGCGCGCGCTGTCGCGCGCGTCACTACCGCGCGCAAGCGACGCT	674
DB	323	CTTCTGTGTCGCGCGCGCGCGCTGTCGCGCGCGTCACTACCGCGCGCAAGCGACGCT	382
QY	675	GGAAGCGCGCGCTGTGAGCGCGCTGTACCGGATGGCGAGCGGTGTGTACTTCCAGTCCGT	734
DB	383	GGAAGCGCGCGCTGTGAGCGCGCTGTACCGGATGGCGAGCGGTGTGTACTTCCAGTCCGT	442
QY	735	GTTGCGCGCGCTACCTCTCATCTCTGTGTGCGCGCGCTCCTCTCTCGCGCGCAATGAGCTTCT	794
DB	443	GTTGCGCGCGCTACCTCTCATCTCTGTGTGCGCGCGCTCCTCTCTCGCGCGCAATGAGCTTCT	502
QY	795	GGCGTGAATGATCTTCGTCGCGCTTCGCTCACTTCTCTTCAACCGTTCGCGCGCTTCTC	854
DB	503	GGCGTGAATGATCTTCGTCGCGCTTCGCTCACTTCTCTTCAACCGTTCGCGCGCTTCTC	562
QY	855	CCTCTGGGCGCGCGCTTCTCTTCTCACTGAGGCGCTCATGCACTACGCGCGCTTACGT	914
DB	563	CGTGTGGGCGCGCGCTTCTCTTCTCACTGAGGCGCTCATGCACTACGCGCGCTTACGT	622
QY	915	CATCACTCTTCGCGCGCGCTTCACTGCGCGCTTACGCGCGCTTACGCGCGCTTACGCGCGCTTACG	974

Db 623 CATCCACATCCCGCGCGTGCCTTCAACCGCGGCTACTGGGTGCGGCAAGAC 682
Qy 975 C 975
Db 683 C 683

RESULT 8
AB083582 1577 bp mRNA linear PLN 07-MAR-2003
LOCUS Oryza sativa (japonica cultivar-group) OsAMT2;2 mRNA for ammonium transporter, complete cds.
AB083582
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
JOURNAL
TITLE
2 (bases 1 to 1577)
Submitted (11-APR-2002) Toshihiko Hayakawa, Tohoku University, Graduate School of Agricultural Science, Department of Applied Plant Science, Laboratory of Plant Cell Biochemistry, Tezumi-dori-Akamiyamachi 1-1, Aoba-ku, Sendai, Miyagi 981-8555, Japan [E-mail: toshi@biochem.tohoku.ac.jp, Tel: 81-22-717-8789, Fax: 81-22-717-8789]
Location/Qualifiers
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/cultivar="Sasanishiki1"
/db_xref="taxon:39947"
/clone="OsAMT2;2"
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1. 1577
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1. 37
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38. 1534
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/product="ammonium transporter"
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ORIGIN
3' UTR
12.3%; Score 454; DB 4; Length 1577;
Best Local Similarity 81.9%; Pired. No. 5.5e-89;
Matches 555; Conservative 0; Mismatches 105; Indels 18; Gaps 2;
300 GATGCTGTCGCGGCGAGCGGTGTCGCGGTACGACGAGGAGACAGTCGCGCTCGGT 359

Db 37 GATGTCGGGGGACGCGTTCAACATGTCGGTGGCCGACACGCG---TCGGGGATGCGCGT 93
Qy 360 GCGGACCTGCTGTAACAAAGGGGAGACAAAGCTGGACAGTGGTGGCGGAGAGCTGTGGG 419
Db 94 GCGGAGTGGCTGAACAAAGGGGAGACAAAGCTGGAGATGATCTTCGGGAGAGCTGTGGG 153
Qy 420 GCTGACAGACGTCGCGGCTGTGTGTGCTGTACGAGCGGCTGTGTGAAGAAAGTGGG 479
Db 154 GATGACAGACGTCGCGGCTGTGTGTGCTGTACGAGCGGCTGTGTGAAGAAAGTGGG 213
Qy 480 GGTGAACCTGCGGCTGTGTGTGCTGTACGAGCGGCTGTGTGAAGAAAGTGGG 539
Db 214 GGTGAACCTGCGGCTGTGTGTGCTGTACGAGCGGCTGTGTGAAGAAAGTGGG 273
Qy 540 CTGGGCGCTACAAACATGTCGTCGCGGAGACGCTCTCCGATCTGGGGGAAAGCGCGGCG 599
Db 274 CTGGGCGCTACAAACATGTCGTCGCGGAGACGCTCTCCGATCTGGGGGAAAGCGCGGCG 333
Qy 600 GCGGCTGACACAGGCGCTCTGTGTGCGCGGCGCGGCTGCGGAGAGCTGCACT--- 655
Db 334 GCGGCTGACACAGGCGCTCTGTGTGCGCGGCGCGGCTGCGGAGAGAGCTGCACT 393
Qy 656 -----ACCGCGCGACGCGAGCGCTGAGACGCGGCGGCTGAGCGGCTGTACC 704
Db 394 CAAGGCGGCGGCGCGCGCGCGAGCGCGCTGTGAGACGCGCATGAGTGAACCGGCTTACCC 453
Qy 705 CATGCGGACGAGTGTGTGTCCTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 764
Db 454 GATGCGCACCATGAGT 513
Qy 765 GCGGCTGCTGCTGCGGCGGCGCATGAGCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 824
Db 514 GCGGCTGCTGCTGCGGCGGCGCATGAGCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 573
Qy 825 CACCTTCTCTTACACGCTGT 884
Db 574 CACCTTCTCTTACACGCTGT 633
Qy 885 GGGCGCTCATGACATCTGCGGCGGCGTACATCCAGCTTCCGCGGATGCGCGGCTT 944
Db 634 GGGGCTCATGACATCTGCGGCGGCGTACATCCAGCTTCTGTGTGTGTGTGTGTGTGTGTGT 693
Qy 945 CACCGCGGCTTACTGGGT 962
Db 694 CACCGCGGCTTACTGGGT 711

RESULT 9
AKI20352 4067 bp mRNA linear PLN 29-OCT-2003
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:J01306B21, full insert sequence.
AKI20352
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1. The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Ohtsuki, K., Shishiki, T., Ohneda, E., Yahagi, M., Suzuki, K., Li, C., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Naitkawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,

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Query Match	12.3%;	Score 454;	DB 4;	Length 110000;
Best Local Similarity	81.9%;	Pred. No. 5.1e-89;		
Matches 555;	Conservative 0;	Mismatches 105;	Indels 18;	Gaps 2;
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AP008207_182	18200001	18310000		
AP008207_183	18300001	18410000		
AP008207_184	18400001	18510000		
AP008207_185	18500001	18610000		
AP008207_186	18600001	18710000		
AP008207_187	18700001	18810000		
AP008207_188	18800001	18910000		
AP008207_189	18900001	19010000		
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AP008207_191	19100001	19210000		
AP008207_192	19200001	19310000		
AP008207_193	19300001	19410000		
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AP008207_195	19500001	19610000		
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Db		28895	CAAGGCGCGCGCGCGCCGACCGCCGACCGCCGTGTGTGAACAACCGCATGGTTGAACCCGCTTAACC	2895
OY		705	GATGGCGCAGCGGTGTGTACTTCACATGCGATTTCGCCGCATCACCCCTCATCTCGTGCG	764
Db		28955	GATGGCCACCATGGTTGTACTTCACATGCGATTTCGCCGCATCACCCCTCATCTCGTGCG	2901
OY		765	CGGCTCCCTCCTCGGCGGCATGAGCTTCTCGCTGATGTATCTTGGTCCGCTGTGGCT	824
Db		29015	CGGCTCGCTGTGGGGGCGGATGAACATCAAGGCGCTGTGATCTGTTCCTCCGCTCTGGCT	2907
OY		825	CACCTTCTCTCAKACCGTCGGCGGCTTCTCCTCTGGGGGGGCGGCGCTTCCCTTTCACACTG	884
Db		29075	CACCTTCTCTCAKACCGTCGGCGGCTTCTCCTCTGGGGGGGCGGCGCTTCTCTTTCACACTG	2913
OY		885	GGGGGTCATGACATCTACGCGCGCGGCTACGTCATCAAGTCCTCGCGCGGCATATCGCGGCTT	944
Db		29135	GGGGGTCATGACATCTACGCGCGCGGCTACGTCATCAAGTCCTCGCGGCGGCATATCGCGGCTT	2919
OY		945	CACCGCGGCTTACTGTGGGT 962	
Db		29195	CACCGCGGCGTACTGTGGGT 29212	
RESULT 11				
AP003235		148892 bp	DNA	linear
DEFINITION		Oryza sativa (japonica cultivar-group)	genomic DNA,	chromosome 1,
LOCUS		Pf.C1 clone:P0039A07.		
ACCESSION		AP003235 BA000010		
VERSION		AP003235.2	GI:13699092	
SOURCE				
ORGANISM		Oryza sativa (japonica cultivar-group)		
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP		
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		Sasaaki,T., Matsumoto,T., Yamamoto,K., Sakata,K., Baba,T.,		
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		Yano,M., Jiang,J., and Gojobori,T.		
		The genome sequence and structure of rice chromosome 1		
		Nature 420 (6913), 312-316 (2002)		
TITLE		2 (bases 1 to 148892)		
JOURNAL		Sasaaki,T., Matsumoto,T. and Yamamoto,K.		
PUBLISHED		Direct Submission		
AUTHORS		Submitted (19-FEB-2001) Takuji Sasaki, National Institute of		
REFERENCE		Agrobiological Sciences, Rice Genome Research Program; Kannondai		
		2-1-2, Tenkuba, Ibaraki, 305-8602, Japan		
		(E-mail:sasakia@affrc.go.jp, URL:http://rpg.dna.affrc.go.jp/,		
		Tel:81-298-38-7441, Fax:81-298-38-7468)		
COMMENT		On Apr 19, 2001 this sequence version replaced gi:13027265.		
		GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENSH		
		(http://www.softberry.com/), GeneMark (http://opal.biology.gatech.edu/GeneMark/), Glimmer		
		(http://www.tigr.org/cdb/glimmer/glmr.form.html), RICEHMM		
		(http://rpg.dna.affrc.go.jp/RICEHMM/), SplicePredictor		
		(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4		

(<http://www.tigr.org/software/glimmer/>), BLASTn and BLASTx. The genomic sequence was searched against NCBI Nonredundant Protein database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database at RGP or DDBJ. Protein homologues of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identical or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-', and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to JRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0039A07 clone has an overlap with P0677H08 (DDBJ: AP003286) clone at 5' end and an overlap with P0491F11 (DDBJ: AP004669) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/genomeseg.html>.

FEATURES

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RESULT 15
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LOCUS Oryza sativa (japonica cultivar-group) chromosome 5 clone
DEFINITION OJ1058.C01, complete sequence.
ACCESSION AC112159
VERSION AC112159.2 GI:38146013
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Euphorbiaceae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
1 (bases 1 to 114236)
Chow, Y.-Y., Hsing, Y.-I. C., Chen, C.-S., Chen, H.-H., Liu, S.-M., Chao, Y.-T., Chang, S.-J., Chen, H.-C., Chen, S.-K., Chen, T.-R., Chen, Y.-L., Cheng, C.-H., Chung, C.-I., Han, S.-Y., Hsieh, S.-H., Hsieh, J.-N., Hsu, C.-H., Huang, J.-J., Kuo, P.-I., Lee, M.-C., Liu, H.-L., Li, Y.-F., Lin, S.-J., Lin, Y.-C., Wu, S.-W., Yu, C.-Y., Yu, S.-W., Wu, H.-P. and Shaw, J.-F.
Oryza sativa BAC OJ1058_C01 genomic sequence

JOURNAL
TITLE
2 (bases 1 to 114236)
Unpublished
Chow, T.-Y. and Hsing, Y.-I. C.
Direct Submission
Submitted (20-FEB-2002) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
3 (bases 1 to 114236)
Hsing, Y.-I. C. and Chow, T.-Y.
Direct Submission
Submitted (29-MAR-2003) Institute of Botany, Academia Sinica, 128, Section 2, Yien-chu-yuan Road, Nankang, Taipei 11529, Taiwan
4 (bases 1 to 114236)
Chow, T.-Y.
Direct Submission
Submitted (03-NOV-2003) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
5 (bases 1 to 114236)
Chow, T.-Y. and Hsing, Y.-I. C.
Direct Submission
Submitted (17-JUN-2004) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
On Nov 3, 2003 this sequence version replaced gi:18767243.
The nucleotide sequence of this BAC clone was generated by combining Monarto and ASPEC-Taiwan sequencing data. The orientation of the sequence is from Sp6 to T7 of the BAC clone.
Genes were predicted from the integrated results of the following: BLASTN2.0, BLASTX2.0, GENSCAN (Chris Burge, <http://genes.mit.edu/GENSCAN.html>), Genshes (<http://www.softberry.com/>), glimmer (<http://www.tigr.org/softlab/glimmer/glimmer.html>), TWINSCAN (<http://www.tigr.org/softlab/glimmer/glimmer.html>) and Genesplizer (<http://www.tigr.org/tcb/Genesplizer/index.shtml>). The sequence was searched against the Swiss-Prot+TrEMBL protein database, the NCBI plant EST database, the TIGR Rice Gene Index and the rice full-length cDNA database (KOME, <http://cdna01.dna.affrc.go.jp/cDNA/>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. This clone overlaps with OJ1387_F08 (accession # AC108503) and OSJNB0005E20 (accession # AC121364).
Location/Qualifiers

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Job time : 20343 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2006, 19:24:01 ; Search time 2149 Seconds
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11929.715 Million cell updates/sec

Title: US-10-713-648a-29

Perfect score: 3677
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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13: geneseqn2004bs.*
14: geneseqn2005s.*
15: geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	662	18.0	1437	12	ADP09655 Rice ammo
3	529.2	14.4	1656	8	AL53990 CDNA enco
4	529.2	14.4	1656	15	AEF16013 Trilicium
5	453.6	12.3	978	11	ACL30507 Rice abio
6	453	12.3	978	11	ACL28101 Rice abio
7	417.4	11.4	1664	13	AD52363 Plant ful
8	389.2	10.6	1883	8	AL53988 CDNA enco
9	389.2	10.6	1883	8	AEF1609 Oryza sat
10	312	8.5	401	12	ADP09621 Rice ammo
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12	289.6	7.9	1961	15	AEF16011 Glycine m
13	279.6	7.6	977	11	ACL28017 Rice abio
14	269	7.3	796	13	AD53169 Plant ful
15	248.2	6.8	974	13	AD53259 Plant ful
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ALIGNMENTS

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AC	ADP09638;	
DT	26-AUG-2004	(first entry)
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XX		
KW	Rice; ammonium transporter; GUS; insertional mutagenesis;	
KW	beta-glucuronidase; biotic stress resistance; pesticide; herbicide;	
KW	plant; ds; hygromycin phosphotransferase; HGH; T-DNA; transfer-DNA.	
XX		
OS	Oryza sativa.	
XX		
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FT	misc_feature	2301..2302
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FT		/note= "Location of T-DNA insert in rice line IC-109-35"
XX		
PN	WO2004046357-A1.	
XX		
PD	03-JUN-2004.	
XX		
PF	14-NOV-2003; 2003WO-KR002461.	
XX		
PR	15-NOV-2002; 2002US-0427166P.	
XX		
PA	(POSC-) POSCO.	
XX	(POST-) POSTECH FOUND.	
XX		
PI	An G, Ryu C, Han J, Kang H, An K;	
XX		
DR	WPI: 2004-449751/42.	
XX	F-PSDB; ADP09672.	
XX		
PT	New organ preferential nucleic acids and polypeptides, useful in	
PT	producing rice plants with desired characteristics and which are	
PT	resistant to herbicide, plant pathogen, fungi, bacteria, virus, insect,	
PT	nematode, and stress.	

XX Claim 1; SEQ ID NO 29; 296bp; English.

PS This invention relates to a novel method of identifying nucleic acid
XX molecules, or fragments thereof, that are expressed in an organ
CC preferential manner in rice. Specifically, it refers to producing rice
CC cell lines that carry tagged genes modified by T-DNA/GUS based
CC insertional mutagenesis, where the GUS portion of the insert is the
CC promoterless beta-glucuronidase reporter gene that can only be expressed
CC when it is inserted into an active gene. The present invention describes
CC generating transformed rice lines containing transfer-DNA (T-DNA)
CC hygromycin phosphotransferase (HPT). Accordingly, this method can be used
CC to produce rice plants with desirable characteristics including increased
CC grain yield and nutritional content, resistance to biotic stresses,
CC pesticides, herbicides or insects, altered morphology or improved
CC characteristics referring to shape, taste or cooking quality of the
CC grain. This polynucleotide sequence represents the genomic DNA of a rice
CC gene that will be T-DNA/GUS tagged for expression analyses, given in an
CC exemplification of the invention.

XX Sequence 3677 BP; 912 A; 920 C; 844 G; 1001 T; 0 U; 0 Other;

Query Match 100.0%; Score 3677; DB 12; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAATTTAAACATAGTCAGCATTAATACATTCATGTTTATCATATTATTAACATA 60
DB 1 AAAATTTAAACATAGTCAGCATTAATACATTCATGTTTATCATATTATTAACATA 60
QY 61 AAATCTAATGTTTAAAGTTTAAATTAACGACATCAAAATTGACATGGAAT 120
DB 61 AAATCTAATGTTTAAAGTTTAAATTAACGACATCAAAATTGACATGGAAT 120
QY 121 TATGTTGAAATGAGGACAGAGGAGTACAGTACAGGCTACTAGCCACGATCAAAAT 180
DB 121 TATGTTGAAATGAGGACAGAGGAGTACAGTACAGGCTACTAGCCACGATCAAAAT 180
QY 181 GGTAAATCGATGCGCACTGACACATGATCCTCTCTATATTAAGTCCCTTAATAC 240
DB 181 GGTAAATCGATGCGCACTGACACATGATCCTCTCTATATTAAGTCCCTTAATAC 240
QY 241 TAGCTAAGATATCAAAAGAAAGGACATCAAGCTTAGTGTGTAATCAAGAGAAAG 300
DB 241 TAGCTAAGATATCAAAAGAAAGGACATCAAGCTTAGTGTGTAATCAAGAGAAAG 300
QY 301 ATGTGTCGTCCGCGACGCTGAGTGCCTGCTGAGCTACAGAGGAAACAATCGGCTG 360
DB 301 ATGTGTCGTCCGCGACGCTGAGTGCCTGCTGAGCTACAGAGGAAACAATCGGCTG 360
QY 361 GCGAAGTGGCTGAACAAGGGGGAACAAGCTGAGCTGAGTGGCGGCGATGAGG 420
DB 361 GCGAAGTGGCTGAACAAGGGGGAACAAGCTGAGCTGAGTGGCGGCGATGAGG 420
QY 421 CTGCAAGAGCTCCGCGCTGAGTGTGTAAGCTGAGTGTGTAAGAAAGTGGG 480
DB 421 CTGCAAGAGCTCCGCGCTGAGTGTGTAAGCTGAGTGTGTAAGAAAGTGGG 480
QY 481 GTGAAGTCCGCGCTTCAAGCTGATGAGCTTCCGCGAGTGTGATGCTGAGTCA 540
DB 481 GTGAAGTCCGCGCTTCAAGCTGATGAGCTTCCGCGAGTGTGATGCTGAGTCA 540
QY 541 TGGGCGTACACATGCTGTTGCGGAGAAAGCTCTCCGATCTGGGGGAAAGCGCG 600
DB 541 TGGGCGTACACATGCTGTTGCGGAGAAAGCTCTCCGATCTGGGGGAAAGCGCG 600
QY 601 GGGCTGACCAAGGCTCTCTGTCGCGCGCGCGCTGCGCGGCGATCCATCCAG 660
DB 601 GGGCTGACCAAGGCTCTCTGTCGCGCGCGCGCTGCGCGGCGATCCATCCAG 660
QY 661 GCGGACGCGAGCTGAGACGCGGCGGCTGAGCGCTGACCCGATGCGAGCGAGT 720
DB 661 GCGGACGCGAGCTGAGACGCGGCGGCTGAGCGCTGACCCGATGCGAGCGAGT 720

DB 661 GCGGACGCGAGCTGAGACGCGGCGGCTGAGCGCTGACCCGATGCGAGCGAGT 720
QY 721 TACTTCCAGTGCCTGTTGCGCGCCATCACTCATCTCTGTCGCGGCTCTCTGCG 780
DB 721 TACTTCCAGTGCCTGTTGCGCGCCATCACTCATCTCTGTCGCGGCTCTCTGCG 780
QY 781 CGCATGAGCTTCCGCGCTGATGATCTGTCGCGCTGAGCTCACTTCTCTACACC 840
DB 781 CGCATGAGCTTCCGCGCTGATGATCTGTCGCGCTGAGCTCACTTCTCTACACC 840
QY 841 GTGCGCGCTTCTCCCTGCGGCGCGCTCTCTTCACTGCGGCGTATGATGATG 900
DB 841 GTGCGCGCTTCTCCCTGCGGCGCGCTCTCTTCACTGCGGCGTATGATGATG 900
QY 901 TGGCGGCTACGCTATCCAGTCTCCGCGGCAATCGCGGCTTCAACCGCGTAT 960
DB 901 TGGCGGCTACGCTATCCAGTCTCCGCGGCAATCGCGGCTTCAACCGCGTAT 960
QY 961 GTCCGCTAACAGGCTCATCTTTTGTGCTATATCTATCTATCAGCAGTATTAAT 1020
DB 961 GTCCGCTAACAGGCTCATCTTTTGTGCTATATCTATCTATCAGCAGTATTAAT 1020
QY 1021 TTTCAATCAATAATTTAAAGCTAATTTTGAAGTTTTCATCCGAAGTTATTTTCATC 1080
DB 1021 TTTCAATCAATAATTTAAAGCTAATTTTGAAGTTTTCATCCGAAGTTATTTTCATC 1080
QY 1081 ATTTGTTTGTGCTGCTAAGACCGTATTAAGTTTATTCACAAATTTACTATG 1140
DB 1081 ATTTGTTTGTGCTGCTAAGACCGTATTAAGTTTATTCACAAATTTACTATG 1140
QY 1141 TTTCAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAG 1200
DB 1141 TTTCAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAG 1200
QY 1201 CTCTGACAAAGTATCAATATGATGCTGCGAGTGGGCGGCGGCGGCGGCGG 1260
DB 1201 CTCTGACAAAGTATCAATATGATGCTGCGAGTGGGCGGCGGCGGCGGCGG 1260
QY 1261 AGGAGAGGTTCCGCGCGGCAATATATGCTGACGAGGAGGAGGAGGAGGAGG 1320
DB 1261 AGGAGAGGTTCCGCGCGGCAATATATGCTGACGAGGAGGAGGAGGAGGAGG 1320
QY 1321 ATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
DB 1321 ATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
QY 1381 GCGGCTCTCAACACCAATCATGCAACGCGCATGAGCTCATGCTGGAATGCTCGAC 1440
DB 1381 GCGGCTCTCAACACCAATCATGCAACGCGCATGAGCTCATGCTGGAATGCTCGAC 1440
QY 1441 GTGATCTTCTTCAAGAAAGCCCTCGGCTGCGGCGGCGGCGGCGGCGGCGG 1500
DB 1441 GTGATCTTCTTCAAGAAAGCCCTCGGCTGCGGCGGCGGCGGCGGCGGCGG 1500
QY 1501 GTTTCATCACCCCGCTGAGGAGTCAATATCACTTCACTCAACGAGAAAGAGCTT 1560
DB 1501 GTTTCATCACCCCGCTGAGGAGTCAATATCACTTCACTCAACGAGAAAGAGCTT 1560
QY 1561 ATTAATTAAGTATGCTAATAATTAATTAATTAATTAATTAATTAATTAATTA 1620
DB 1561 ATTAATTAAGTATGCTAATAATTAATTAATTAATTAATTAATTAATTAATTA 1620
QY 1621 AAAATTTGCGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
DB 1621 AAAATTTGCGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
QY 1681 TTGAAGTTGAAAACTGATGACGACAGCTTATATTAATTAATTAATTAATTAAT 1740
DB 1681 TTGAAGTTGAAAACTGATGACGACAGCTTATATTAATTAATTAATTAATTAAT 1740
QY 1741 ACTTAATTAATTTTGGATGATGATGATGATGATGATGATGATGATGATGATG 1800
DB 1741 ACTTAATTAATTTTGGATGATGATGATGATGATGATGATGATGATGATGATG 1800

QY 1801 TCGATTCTTAATTAAGTATTAATCCCGGTTGCGAGATTAATGATCCCTTCCCGCCCAAG 1860
 DB 1801 TCGATTCTTAATTAAGTATTAATCCCGGTTGCGAGATTAATGATCCCTTCCCGCCCAAG 1860
 QY 1861 TTGTTTTGACTTGAATCTTAAGCTGTGCGGTGCGCAACAATACAGAGGTTGGTTACC 1920
 DB 1861 TTGTTTTGACTTGAATCTTAAGCTGTGCGGTGCGCAACAATACAGAGGTTGGTTACC 1920
 QY 1921 TTGCGTCCCAATTAATCTGCAATTTTCCCGTAGAATTAACCGCTTACATTTTGTGCA 1980
 DB 1921 TTGCGTCCCAATTAATCTGCAATTTTCCCGTAGAATTAACCGCTTACATTTTGTGCA 1980
 QY 1981 TTAGCGGCGCAATTAATCTGCAATTTTCCCGTAGAATTAACCGCTTACATTTTGTGCA 1980
 DB 1981 TTAGCGGCGCAATTAATCTGCAATTTTCCCGTAGAATTAACCGCTTACATTTTGTGCA 1980
 QY 1981 CTAAATTAAGCAGCAGCAGCACTGATTTATCATATCTCTCTCACTCTCTTGTAGTGG 2040
 DB 1981 CTAAATTAAGCAGCAGCAGCACTGATTTATCATATCTCTCTCACTCTCTTGTAGTGG 2040
 QY 2041 AAGAGTCGTAAGTTTCTCATCTCTTGTGCAAGTTGTGATGATGATGATGATGATGATGAT 2100
 DB 2041 AAGAGTCGTAAGTTTCTCATCTCTTGTGCAAGTTGTGATGATGATGATGATGATGATGAT 2100
 QY 2101 TTAATTTCCGTCACATGCTACATGACATCTAATGTGAACAATACAAACGTTCAATCGG 2160
 DB 2101 TTAATTTCCGTCACATGCTACATGACATCTAATGTGAACAATACAAACGTTCAATCGG 2160
 QY 2161 AATCTAGGTTGGTGTGATGATACATATTTTGTGCGCAACGAGAAATCTTATTTGTGCTT 2220
 DB 2161 AATCTAGGTTGGTGTGATGATACATATTTTGTGCGCAACGAGAAATCTTATTTGTGCTT 2220
 QY 2221 GGGCTTAATGCTAATGAGCAATCTTATCACTAGCTGTGATGATGATGATGATGATGATGAT 2280
 DB 2221 GGGCTTAATGCTAATGAGCAATCTTATCACTAGCTGTGATGATGATGATGATGATGATGAT 2280
 QY 2281 TCTGAAACTGCCAATTTGTTTTTCTGAGTTTTTCTGTAGCGCAGCAGCAAGAAAAG 2340
 DB 2281 TCTGAAACTGCCAATTTGTTTTTCTGAGTTTTTCTGTAGCGCAGCAGCAAGAAAAG 2340
 QY 2341 CACACTGAAATGAAAGTGAATATTTTACAGCTTCCCATTCCTGCGGAGCTTCCTTCA 2400
 DB 2341 CACACTGAAATGAAAGTGAATATTTTACAGCTTCCCATTCCTGCGGAGCTTCCTTCA 2400
 QY 2401 AAGTCAATTAAGCGCGGAGATGAGCTACAGTACTCAGTACATGATGATGATGATGATGATGAT 2460
 DB 2401 AAGTCAATTAAGCGCGGAGATGAGCTACAGTACTCAGTACATGATGATGATGATGATGATGAT 2460
 QY 2461 GGCACGTGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2520
 DB 2461 GGCACGTGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2520
 QY 2521 TACACCCCTTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2580
 DB 2521 TACACCCCTTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2580
 QY 2581 TACACCCCTTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2640
 DB 2581 TACACCCCTTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2640
 QY 2641 TTTTGGTATCAAAACATGATTAATTTTGTGCTGATGATGATGATGATGATGATGATGATGAT 2700
 DB 2641 TTTTGGTATCAAAACATGATTAATTTTGTGCTGATGATGATGATGATGATGATGATGATGAT 2700
 QY 2701 CATTTTAAATTTCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2760
 DB 2701 CATTTTAAATTTCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2760
 QY 2761 TTTTAAATTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 2820
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QY 2881 CAGGGGTGATGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGAT 2940
 DB 2881 CAGGGGTGATGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGAT 2940
 QY 2941 GGTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
 DB 2941 GGTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
 QY 3001 TGGGGTCTTCCAC 3060
 DB 3001 TGGGGTCTTCCAC 3060
 QY 3061 TGGGGTCTTCCAC 3120
 DB 3061 TGGGGTCTTCCAC 3120
 QY 3121 ACGGGGCG 3180
 DB 3121 ACGGGGCG 3180
 QY 3181 CCTGGAACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 3240
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 QY 3241 GATGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 3300
 DB 3241 GATGCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 3300
 QY 3301 CGCTCGGGGCG 3360
 DB 3301 CGCTCGGGGCG 3360
 QY 3361 CCGCTCGGGGCG 3420
 DB 3361 CCGCTCGGGGCG 3420
 QY 3421 AAGAAATTCATAC 3480
 DB 3421 AAGAAATTCATAC 3480
 QY 3481 AATCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 3540
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 DB 3541 TTTGCAATTCAGGAGAGTCCGCTCTGATTTTGTGATTTGTAATTAATTAATTAATTAATTAAT 3600
 QY 3601 TTTTGAATTCCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 3660
 DB 3601 TTTTGAATTCCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAATGCTAAT 3660
 QY 3661 CTCATATTTTCCAAA 3677
 DB 3661 CTCATATTTTCCAAA 3677
 RESULT 2
 ADP09655
 ID ADP09655 strand: DNA; 1437 BP.
 AC ADP09655;
 DT 26-AUG-2004 (first entry)
 XX
 DE Rice ammonium transporter ORF DNA without the T-DNA insert SegID 46.
 XX
 KW rice; ammonium transporter; GUS; insertional mutagenesis;
 KW beta-glucuronidase; biotic stress resistance; pesticide; herbicide;
 KW plant; ds; hygromycin phosphotransferase; Hdh; T-DNA; transfer-DNA; gene.
 XX
 OS Oryza sativa.
 XX

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FH Key Location/Qualifiers
FT CDS 1..1437
FT /*tag=a
FT /product="Rice protein"
PN MO2004046357-A1.
XX
XX 03-JUN-2004.
XX
XX 14-NOV-2003; 2003WO-KR002461.
XX
XX 15-NOV-2002; 2002US-0427166P.
XX
XX (POSC-) POSCO.
XX (POST-) POSTECH FOUND.
XX
XX An G, Ryu C, Han J, Kang H, An K,
XX
XX MPI; 2004-449751/42.
XX
XX P-PSDB; ADP09672.
XX
XX New organ preferential nucleic acids and polypeptides, useful in
XX producing rice plants with desired characteristics and which are
XX resistant to herbicide, plant pathogen, fungi, bacteria, virus, insect,
XX nematode, and stresses.
XX
XX Claim 8; SEQ ID NO 46; 296pp; English.
XX
XX This invention relates to a novel method of identifying nucleic acid
XX molecules, or fragments thereof, that are expressed in an organ
XX preferential manner in rice. Specifically, it refers to producing rice
XX cell lines that carry tagged genes modified by T-DNA/GUS based
XX insertional mutagenesis, where the GUS portion of the insert is the
XX promoterless beta-glucuronidase reporter gene that can only be expressed
XX when it is inserted into an active gene. The present invention describes
XX generating transformed rice lines containing the selectable marker
XX GUS. This also carry a gene encoding the selectable marker
XX hygromycin phosphotransferase (Hph). Accordingly, this method can be used
XX to produce rice plants with desirable characteristics including increased
XX grain yield and nutritional content, resistance to biotic stresses,
XX pesticides, herbicides or insects, altered morphology or improved
XX characteristics referring to shape, taste or cooking quality of the
XX grain. This polynucleotide sequence represents the open reading frame DNA
XX of a rice gene that will be T-DNA/GUS tagged for expression analyses,
XX given in an exemplification of the invention.
XX
XX Sequence 1437 BP; 193 A; 514 C; 470 G; 260 T; 0 U; 0 Other;
XX
XX Query Match 18.0%; Score 662; DB 12; Length 1437;
XX Best Local Similarity 99.3%; Pred. No. 3.1e-91;
XX Matches 665; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 301 ATGTGTCGTCCGCGACGCGTGTGCGCTGCGCTACACAGGGAACAAGTCGCGCTGCGTG 360
XX 1 ATGTGTCGTCCGCGACGCGTGTGCGCTGCGCTGCGCTACACAGGGAACAAGTCGCGCTGCGTG 60
XX
XX 361 GCGGACTGCGCTGACAAAGGGAAGGGAACAAGCGGTGCGACGCTGCGCGGCGGCGGCGGCGG 420
XX 61 GCGGACTGCGCTGACAAAGGGAAGGGAACAAGCGGTGCGACGCTGCGCGGCGGCGGCGGCGG 120
XX
XX 421 CTGCAGAGCGTGC CGCGGCTTGTGTGCTGTACCGCGCGCGTGTGTAAGAAAGTGGCGG 480
XX 121 CTGCAGAGCGTGC CGCGGCTTGTGTGCTGTACCGCGCGCGTGTGTAAGAAAGTGGCGG 180
XX
XX 481 GTGAAGCTGGCGCTTACGCGCTTTCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 540
XX 181 GTGAAGCTGGCGCTTACGCGCTTTCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 240
XX
XX 541 TGGGCGTACCAATGCTGCTTGGGGAAGAGCTCTCCGATCTTGGGGAAGAGCGCGCGCGG 600
XX 241 TGGGCGTACCAATGCTGCTTGGGGAAGAGCTCTCCGATCTTGGGGAAGAGCGCGCGCGG 300
XX
XX 601 GCGCTGAGACAGGCGCTCTCGTGGGCGCGCGCGCTGCGCGGACGCTGCACTACCGCG 660

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DB 301 GCGCTGAGACAGGCGCTCTCGTGGCGCGCGCGCTGCGCGGAGACGCTCACCTACCGC 360
XX
XX 661 GCCACGCGACGCTGAGAGACGCGCGCGTGGAGCGCGCTGACCGGATGGCGAGCGTGGTG 720
XX
XX 361 GCCACGCGACGCTGAGAGACGCGCGCGTGGAGCGCGCTGACCGGATGGCGAGCGTGGTG 420
XX
XX 721 TACTTCAGTGCAGTGTGGCGCGCATACCTCAATCCCTGTCGCGCGCTCCCTCTCGGC 780
XX 421 TACTTCAGTGCAGTGTGGCGCGCATACCTCAATCCCTGTCGCGCGCTCCCTCTCGGC 480
XX
XX 781 CGCATGAGCTTCTTCGCGCTGATGATCTTGTCCGCTTGGCTTACCTTCTCTACAC 840
XX 481 CGCATGAGCTTCTTCGCGCTGATGATCTTGTCCGCTTGGCTTACCTTCTCTACAC 540
XX
XX 841 GTGCGCGCGCTTCTCCCTTGGGCGCGCGCTTCCCTTCCACTGAGGCGTATGACATAC 900
XX 541 GTGCGCGCGCTTCTCCCTTGGGCGCGCGCTTCCCTTCCACTGAGGCGTATGACATAC 600
XX
XX 901 TCGGCGGCTACGCTATCAGCTCTCCGCGGAGATCGCGGCTTACACCGCGCTTACTG 960
XX 601 TCGGCGGCTACGCTATCAGCTCTCCGCGGAGATCGCGGCTTACACCGCGCTTACTG 660
XX
XX 961 GTCCGCTACTA 970
XX
XX 661 GTGGGGCCAA 670
XX
XX
XX RESULT 3
XX AAL53990
XX ID AAL53990 standard; cDNA; 1656 BP.
XX
XX AAL53990;
XX
XX 18-FEB-2003 (first entry)
XX
XX cDNA encoding a wheat high affinity ammonium transporter protein #2.
XX
XX Herbicide; ammonium transporter protein; herbicide; transgenic plant;
XX wheat; gene; ss.
XX
XX Triticum aestivum.
XX
XX Key Location/Qualifiers
XX FT 93..1505
XX FT /*tag=a
XX FT /product="wheat high affinity ammonium transporter
XX protein"
XX
XX US2002142390-A1.
XX
XX 03-OCT-2002.
XX
XX 28-DEC-2001; 2001US-00033109.
XX
XX 28-AUG-1998; 98US-0098248P.
XX
XX 27-AUG-1999; 99US-00384625.
XX
XX (ALLE/) ALLEN S M.
XX
XX (RAFA/) RAFALSKI J A.
XX
XX Allen SM, Rafalski JA;
XX
XX MPI; 2003-102520/09.
XX
XX P-PSDB; MA026538.
XX
XX Novel ammonium transporter polypeptide useful for identifying enzymatic
XX inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
XX transporter polypeptides.
XX
XX Claim 3; Page 23-24; 27pp; English.
XX
XX The invention relates to a novel ammonium transporter protein comprising

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90% homology based on the Clustal method compared to: a corn ammonium transporter polypeptide of 183 or 63 amino acids; a soybean ammonium transporter polypeptide of 500 or 486 amino acids; a wheat ammonium transporter polypeptide of 494 or 470 amino acids; and a rice ammonium transporter 497 amino acids fully defined in the specification. The isolated polynucleotide is useful for selecting an isolated polynucleotide that affects the level of expression of the ammonium transporter polypeptide in a plant cell. The ammonium transporter protein is useful for preparing antibodies which are useful for detecting the transporter protein in situ in cells or in vitro in cell extracts, and as targets to facilitate design and/or identify inhibitors of the enzymes that are useful as herbicides. The isolated polynucleotide is also useful for creating transgenic plants in which the polynucleotide is present at higher or lower levels than normal, and for designing and producing primer pairs which are useful in amplification or primer extension reactions. This polynucleotide sequence represents the cDNA encoding a wheat high affinity ammonium transporter protein of the invention

Sequence 1656 BP; 262 A; 532 C; 520 G; 342 T; 0 U; 0 Other;

Query Match 14.4%; Score 529.2; DB 8; Length 1656;

Best Local Similarity 86.9%; Pred. No. 4.7e-71; Matches 582; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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QY 306 GTGCTGAGGAGCGTGTGCGCTGCGTACGAGGGAACAGTGGCGTGGGCGGA 365
DB 83 GTGGGCAAGATGTCGTGCGGTGCGTACGAGGGAACAGTGGCGTGGGCGGA 142
QY 366 CTGGCTGAACAAGGAGGAGCAACGCTGAGAGTGTGGCGGCGAGCTGGGAGCTGCA 425
DB 143 CTGGCTGAACAAGGAGGAGCAACGCTGAGAGTGTGGCGGCTGCAAGCTGGGAGCTCA 202
QY 426 GAGCGTCCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 485
DB 203 GAGCGTCCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 262
QY 486 CTGGCGTTCATGGGCGCTCTACGCGCTTCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 545
DB 263 CTGGCGTTCATGGGCGCTCTACGCGCTTCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 322
QY 546 GTACAACATGTCTGTGGGAGAGAGTCTCCGATCTGGGAGAGAGCGCGCGCGCT 605
DB 323 CTACAACATGTCTGTGGGAGAGAGTCTCCGATCTGGGAGAGAGCGCGCGCGCT 382
QY 606 GAGCAGGAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 665
DB 383 GAGCAGGAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 442
QY 666 CGGCAAGCTGTGAGACGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
DB 443 CGGCAAGCTGTGAGACGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 502
QY 726 CCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 785
DB 503 CCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 562
QY 786 GAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 845
DB 563 GAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 622
QY 846 CGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 905
DB 623 CGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 682
QY 906 CGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 965
DB 683 CGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 742
QY 966 TACTAAAGC 975
DB 743 GCCAAGAGC 752

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RESULT 4

AEF16013
ID AEF16013 standard; cDNA; 1656 BP.

AC AEF16013;

DT 09-MAR-2006 (first entry)

DE Triticum aestivum ammonium transporter cDNA Segid13.

KW ammonium transfer; transgenic plant; nitrogen; cellular transport; gene;

OS Triticum aestivum.

EH Key Location/Qualifiers

FT CDS 93..1505

FT /tag= a

PN US2006010512-A1.

PD 12-JAN-2006.

PF 15-DEC-2004; 2004US-00012668.

PR 28-DEC-2001; 2001US-00033109.

PA (ALIE/) ALLEN S M.

PI (RAFA/) RAFALSKI J A.

PI Allen SM, Rafalski JA;

DR WPI; 2006-088761/09.

DR P-PSDB; AEF16014.

PT New isolated polynucleotide encoding a polypeptide having ammonium transfer activity; useful for producing transgenic plants with increased nitrogen content.

PS Disclosure; SEQ ID NO 13; 29pp; English.

CC This invention relates to a novel isolated polynucleotide encoding a polypeptide having ammonium transfer activity. The polynucleotides are

CC useful for producing transgenic plants with increased nitrogen content.

CC The present sequence is a cDNA homologous to the sequence of the

CC invention which encodes an ammonium transporter.

XX Sequence 1656 BP; 262 A; 532 C; 520 G; 342 T; 0 U; 0 Other;

Query Match 14.4%; Score 529.2; DB 15; Length 1656;

Best Local Similarity 86.9%; Pred. No. 4.7e-71; Matches 582; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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QY 306 GTGCTGAGGAGCGTGTGCGCTGCGTACGAGGGAACAGTGGCGTGGGCGGA 365
DB 83 GTGGGCAAGATGTCGTGCGGTGCGTACGAGGGAACAGTGGCGTGGGCGGA 142
QY 366 CTGGCTGAACAAGGAGGAGCAACGCTGAGAGTGTGGCGGCGAGCTGGGAGCTGCA 425
DB 143 CTGGCTGAACAAGGAGGAGCAACGCTGAGAGTGTGGCGGCTGCAAGCTGGGAGCTCA 202
QY 426 GAGCGTCCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 485
DB 203 GAGCGTCCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 262
QY 486 CTGGCGTTCATGGGCGCTCTACGCGCTTCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 545
DB 263 CTGGCGTTCATGGGCGCTCTACGCGCTTCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 322
QY 546 GTACAACATGTCTGTGGGAGAGAGTCTCCGATCTGGGAGAGAGCGCGCGCGCT 605
DB 323 CTACAACATGTCTGTGGGAGAGAGTCTCCGATCTGGGAGAGAGCGCGCGCGCT 382

```

QY 606 GGACCAAGGCTCTCTCTGTCGGCCGCGCCGCTGCGCGAGCGTTCATACCGCGCGCA 665
DB 383 CGACCAAGGCTCTCTCTGTCGGCCGCGCCGCTGCGCGAGCGTTCATACCGCGCGCA 442
QY 666 CGGCAAGCGTGAAGCGCGCGCGTGAAGCGCGTGAAGCGCGTGAAGCGCGTGAAGCG 725
DB 443 CGGCAAGCGTGAAGCGCGCGTGAAGCGCGTGAAGCGCGTGAAGCGCGTGAAGCG 502
QY 726 CCAAGTGGCTGTCGGCGCGCATACCTCTCTCTGTCGGCGCTCTCTCTGCGCGCAT 785
DB 503 CCAAGTGGCTGTCGGCGCGCATACCTCTCTCTGTCGGCGCTCTCTCTGCGCGCAT 562
QY 786 GAGCTTCT 845
DB 553 GAGCTTCT 622
QY 846 CGCTTCT 905
DB 623 CGCTTCT 682
QY 906 CGGCTAAGCTATCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 965
DB 683 CGGCTAAGCTATCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 742
QY 966 TACTAAGACG 975
DB 743 GCCAAGGACC 752

RESULT 5

ID ACL30507 standard; cDNA; 978 BP.

AC 30507;

DT 02-JUN-2005 (first entry)

DE Rice abiotic stress responsive polynucleotide SEQ ID NO:8685.

KW 86; abiotic stress tolerance; transgenic plant; plant; cereal;

KW agriculture.

OS Oryza sativa.

XX WO2003008540-A2.

PD 30-JAN-2003.

PF 21-JUN-2002; 2002WO-US019668.

PR 22-JUN-2001; 2001US-0300112P.

PR 24-AUG-2001; 2001US-0314662P.

PR 26-SEP-2001; 2001US-0325272P.

PR 21-NOV-2001; 2001US-0332132P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Krepes J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Karagiri F,

PI Moughamer T, Provart N, Rieke D, Zhu T;

XX WPI; 2003-248011/24.

XX New stress-responsive nucleic acid, useful for altering the

XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold

XX stress, salt stress or osmotic stress.

XX Claim 1, SEQ ID NO 8685; 89pp; English.

XX The invention relates to novel abiotic stress responsive polynucleotides

XX and polypeptides. Also disclosed are vectors, expression cassettes, host

XX cells, and plants containing such polynucleotides. Also disclosed are

XX methods for using the polynucleotides and polypeptides to alter the

CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention

SQ Sequence 978 BP; 145 A; 321 C; 320 G; 191 T; 0 U; 1 Other;

Query Match 12.3%; Score 453.6; DB 11; Length 978;

Best Local Similarity 81.8%; Pred. No. 1.3e-59;

Matches 554; Conservative 0; Mismatches 105; Indels 18; Gaps 2;

QY 301 ATGTCGTGTCGGCGCAGCGTGTGTCGGCGTGAACAGGAGAACAGCGTGTG 360
DB 1 ATGTCGGGGAGAGCGTTCAACATGTCGGTGAACAGCGG---TGGGGATGGCGGTG 57
QY 361 GCGGACTGCTGAACAGGAGAGAACAGCGTGTGAGCTGTGTGGCGCAAGCTGTGGGG 420
DB 58 CCGGAGTGGCTGAACAGGAGAGAACAGCGTGTGAGATCTGCGCAGCCTGTGTGGGG 117
QY 421 CTGCAAGAGCGTGGCGCGT 480
DB 118 ATGCAAGAGCGTGGCGCGT 177
QY 481 GTGAACCTGCGGCTTCATGAGCGCTCTACAGCTTCGCGCGCGTGTGTGTGTGTGTGTGT 540
DB 178 GTGAACCTGCGGCTTCATGAGCGCTCTACAGCTTCGCGCGCGTGTGTGTGTGTGTGTGT 237
QY 541 TGGGCGTACACATGT 600
DB 238 TGGGCGTACACATGT 297
QY 601 GCGCTGAGACAGGCGCTCTGTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
DB 298 GCGCTGAGACAGGCGCTCTGTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 357
QY 656 -----ACCG 705
DB 358 AAGGCG 417
QY 706 ATGCGAGAGGT 765
DB 418 ATGCGAGAGGT 477
QY 766 GGTCT 825
DB 478 GGTCT 537
QY 826 ACCCTTCTCTACACCGT 885
DB 538 ACCCTTCTCTACACCGT 597
QY 886 GCGCTATGACTATGCGCGCGCTACGTCATCCAGTCTCGCGCGCATCGCGCGCTTC 945
DB 598 GCGCTATGACTATGCGCGCGCTACGTCATCCAGTCTCGCGCGCATCGCGCGCTTC 657
QY 946 ACCGCGGCTTACTGGGT 962
DB 658 ACCGCGGCTTACTGGGT 674

RESULT 6

ID ACL28101 standard; cDNA; 978 BP.

AC 28101;

DT 02-JUN-2005 (first entry)

DJ		Rice	abiotic stress responsive polynucleotide SEQ ID NO:2057.
XX		sb:	abiotic stress tolerance; transgenic plant; plant; cereal;
KM			agriculture.
OS		Oryza sativa.	
XX		MO2003008540-A2.	
PN			
PD		30-JAN-2003.	
XX			
PF		21-JUN-2002; 2002WO-US019668.	
PR		22-JUN-2001; 2001US-0300112P.	
PR		24-AUG-2001; 2001US-0314662P.	
PR		26-SEP-2001; 2001US-0325277P.	
PR		21-NOV-2001; 2001US-0332132P.	
XX		(SYGN) SYNGENTA PARTICIPATIONS AG.	
PA			
PI		Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;	
PI		Moughamer T, Provart N, Ricke D, Zhu T;	
XX			
XX		WPI; 2003-248011/24.	
DR			
PT		New stress-responsive nucleic acid, useful for altering the	
PT		responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold	
PT		stress, salt stress or osmotic stress.	
PS			
XX		Claim 1; SEQ ID NO 2057; 89pp; English.	
XX			
CC		The invention relates to novel abiotic stress responsive polynucleotides	
CC		and polypeptides. Also disclosed are vectors, expression cassettes, host	
CC		cells, and plants containing such polynucleotides. Also disclosed are	
CC		methods for using the polynucleotides and polypeptides to alter the	
CC		responsiveness of a plant to abiotic stress. The invention is useful in	
CC		agriculture. The nucleic acid is useful for determining whether a test	
CC		plant has been exposed to an abiotic stress condition. It is also useful	
CC		for selecting an agent that alters abiotic stress regulated	
CC		polynucleotide expression in a plant cell, and to identify a homolog or	
CC		ortholog to an abiotic stress responsive polynucleotide. The nucleic acid	
CC		molecule and the polypeptide encoded by it are useful in altering the	
CC		responsiveness of a plant to an abiotic stress, such as cold stress, salt	
CC		stress, osmotic stress or any of their combinations. The present sequence	
CC		is used in the exemplification of the invention	
SQ			
XX		Sequence 978 BP; 145 A; 321 C; 320 G; 191 T; 0 U; 1 Other;	
Query Match	12.3%;	Score 453; DB 11; Length 978;	
Best Local Similarity	81.8%;	Pred. No. 1.6e-59;	
Matches	554; Conservative	0; Mismatches 105; Indels 18; Gaps 2	
DJ		301 ATGTCGTCTGGCGACGCGTGTCGCCGTCGATCCAGGGAACAACGTCGCCTTGGTG	360
DB		1 ATGTCGGGGGACGCGCTTCAACATGTCTGGTGGCGTACCAGCCG---TCGGGATGCGCGTG	57
QY		361 GCGGACTGGCTGAAACAAGGGGGCAACGCTGGCAGCTGGTGCGCGCACGCTGGTGGGG	420
DB		58 CCGAGTGGCTGAAACAAGGGGGCAACGCTGGCAGATGATTCCGCGACGCTGGTGGGG	117
QY		421 CTGCAGACGCTGCGCGGCGCTGTGTGTGCTGTACCGCGCGCTGGTAGAAGAAGTGGCG	480
DB		118 ATGCAGACGCTGCCGGGCGCTGTGATCTGTACGCGAGCATGTGAAGAAGAATGGCGG	177
QY		481 GTGAACCTGGCGTTATGCGCGCTTACGCGCTTCCGCGCGCTGTGATCTGTGGGTACCC	540
DB		178 GTGAACCTGGCGTTATGCGCGCTTACGCGCTTCCGCGCGCTGTGATCTGTGGGTACCC	237
QY		541 TGGGGCTAACATGTCTGTGGGGGAAGCTCTCCGATCTGGGGGAAGGCGCGCGCG	600
DB		238 TGGGGCTAACATGTCTGTGGGGGAAGCTCTCCGATCTGGGGGAAGGCGCGCGCG	297

Qy	601	GGCGTGGACCAAGGGGCGCTCTGTGGGCGCGCGCTGGCCGACGATCTCACT-----	655
Db	298	GGCGTGGGACCAAGACTTCTCTCTCGCCGACGCGCTGGCCGACGATCTCACT	357
Qy	656	-----ACCGCGCGACGCGACGCGTGGAGACGCGCGCGGTGGAGCCGCTGTACCG	705
Db	358	AAGGGCGGCGCGCGCGCGCGACGCGCGGTGGAGACGCGATGGGTGAACCGGCTTACCG	417
Qy	706	ATGGCGACGCGTGTGTATCTTCAAGTGGGTGTTCGCGCGCATATCAGCTTATCTGTGCGC	765
Db	418	ATGGCGACGATGTGTATCTTCAAGTGGGTGTTCGCGCGCATATCAGCTTATCTGTGCGC	477
Qy	766	GGCTTCCTCCCGCGCGCGATAGCGTCTGTGCGCGATGATCTTGTGCGCGCTGAGCTC	825
Db	478	GGCTTCGCTCGCGCGCGATAGCATCAAGCGGTGAATGCTGTTCGCGCTGTGAGCTC	537
Qy	826	ACCTTCTCTTACACCGTGGCGCGCTTCTCCCTGTGGGCGCGCGCTTCTTTCATCGG	885
Db	538	ACCTTCTCTTACACCGTGGCGCGCTTCTCCCTGTGGGCGCGCGCTTCTTTCATCGG	597
Qy	886	GGCGTCAATCGACTACTGCGCGCGCTAGCTATCCAGTCTCGCGCGCATGCGCGCTTC	945
Db	598	GGCGTCAATGACTACTCGCGCGCGCTAGCTATCCAGTCTCGCGCGCATGCGCGCTTC	657
Qy	946	ACCGCGCGCTTACTGGGT 962	
Db	658	ACCGCGCGGTACTGGGT 674	
RESULT 7			
ID	ADX52363	standard; cDNA; 1664 BP.	
XX	ADX52363;		
XX	21-APR-2005	(first entry)	
DE	Plant full length insert polynucleotide seqid 27103.		
XX	plant protectant; plant growth regulant; gene therapy; plant;		
KW	recombinant DNA construct; physical array; plant breeding marker;		
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;		
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;		
KW	growth rate; cell cycle pathway; disease resistance;		
KW	galactomannan production; lignin production; plant growth regulator;		
KW	yield; plant growth; plant development; seed oil; protein yield;		
KW	protein content; gene; ss.		
XX	Unidentified.		
OS	US2004034888-A1.		
PN	19-FEB-2004.		
XX	28-APR-2003; 2003US-00425114.		
PF	06-MAY-1999; 99US-00304517.		
XX	05-NOV-2001; 2001US-00985678.		
XX	(LIUJ/) LIU J.		
PA	(ZHOU/) ZHOU Y.		
PA	(KOVA/) KOVALIC D K.		
PA	(SCRE/) SCREEN S E.		
PA	(TABAJ/) TABASKA J E.		
PA	(CAOY/) CAO Y.		
XX			
PI	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;		
XX	WPI; 2004-180133/17.		
PT	New recombinant DNA construct, useful for improving plant tolerance to		
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or		
PT	pests, for conferring increased resistance to plant disease, or for		

[illegible]

XX	(ALLB/) ALLEN S M.
PA	(RAFA/) RAFALSKI J A.
XX	
F1	Allen SM, Rafalski JA;
XX	
DR	WPI; 2006-088761/09.
XX	P-PSDB; ABF1610.
XX	
PT	New isolated polynucleotide encoding a polypeptide having ammonium
PT	transfer activity, useful for producing transgenic plants with increased
PT	nitrogen content.
XX	
PS	Disclosure; SEQ ID NO 9; 29pp; English.
XX	
CC	This invention relates to a novel isolated polynucleotide encoding a
CC	polypeptide having ammonium transfer activity. The polynucleotides are
CC	useful for producing transgenic plants with increased nitrogen content.
CC	The present sequence is a cDNA homologous to the sequence of the
CC	invention which encodes an ammonium transporter.
XX	
SQ	Sequence 1883 BP; 327 A; 592 C; 607 G; 357 T; 0 U; 0 Other;
	Query Match 10.6%; Score 389.2; DB 15; Length 1883;
	Best Local Similarity 74.0%; Pred.No. 8.8e-50;
	Matches 493; Conservative 0; Mismatches 173; Indels 0; Gaps 0;
OY	297 GAAGATGTCGTCTCGTGGCGACGCTGTGTGCCTGACCGAAGGAGAAACAGTGCGCTC 356
Db	74 GAAGAAGTAGATGATGCGCTGCCGACCAGCGGCGCGGCGCTGAATGCGCGCCCAACCGGC 133
OY	357 GGTGGCCGACTCGCTGTAACAAGAGGGGAGAACAGCGTGGACGTGGTGGGGGAGCGCTGGT 416
Db	134 GTTCGCCGAGAGGTGCTGAACACCGGGGACAAAGGGGTGGAGCTCCGGGGCGAGCGTTCTGT 193
OY	417 GGCGCTGAGACGCGCCGGGCTTGTGTGTCTGTACAGCGCGCGTGTGTGAAGAAAGATG 476
Db	194 CGGGCTTCAGTCGATGCTCTGGGCTGTGTGTCTGTACGAGCATCGTGAAGAAAGATG 253
OY	477 GGCAGTGAATCGGCGCTTCATGTGGCGCTTACGCTTCGCGCGCGCTGTGATCTGTGGGT 536
Db	254 GGCGTCAACTCGGCTTCATGTGGCGCTGTACGCTACGCTCACTCATGTGTGGGT 313
OY	537 CACTTGGCGGTGAACAATGTGTTCGGGGAGAAAGTCTCTCCGATCTGGGGAGAGCCGC 596
Db	314 GCTGTGTCGCTTCGCAATGGGCTTCGGGACCGGCTGCTCCGTTCTGGGGAGAGCCGC 373
OY	597 GCCGGCGGTGAACAGAGGCGCTCTGTGTGGCGCGCGCGCGCTGCACGCGGACGCTCACTA 656
Db	374 CGCGGCGGTGAACGAGAGGGGTTCTGTGTGGCGCGCGCGCTGCCGACAGGCGCACTTA 433
OY	657 CCGGCGCGACGAGCGAGCGTGAAGACGCGCGCGGCTGTGAACCCGATGGCGACGAT 716
Db	434 CGGGAAGACGCGGCCCTCTGAGTGGCGCGACGAGCGCTTCAACCGAGGGGTTCAT 493
OY	717 GGTGTACTTCAGTGGCTGTTCGCCGCATCACTCTATCTCGTGGCGCTCTCTCT 776
Db	494 GGTGTGTTCAGTTCGAGCTCGCGCGCATCACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 553
OY	777 CGGCCGATGAGCTTCTCGCGCTGAGATTTGTGTCCCGGCTGAGGCTCACTTCTCGTA 836
Db	554 CGGAGGATGAACATCAAAGGCTGATGGCGTTCACTCGCTCTGTGTCTCTTCTCTTA 613
OY	837 CACGATCGGCGCTTCTCTCTGTGGGGCGGGCTTCTCTTCACTTGGGCGTCACTGA 896
Db	614 CACGCTGTGGCGCTTCAAGCTCTGGGGCGGGGCTTCTCTTCAACAGTGGGGGTATGGA 673
OY	897 CTACTGTGGCGGCTACGTATCACTGTTCGCGCGGATCGCGGCTTCAACCGCGCTTA 956
Db	674 CTACTGTGGCGGATACGTATCACTGTTCCTCGGCGATCGCGGCTTCAACCGCGCTTA 733
OY	957 CTGGGT 962

DB 734 CTGGGT 739

RESULT 10
ADP09621
ID ADP09621 standard; DNA; 401 BP.
XX
AC ADP09621;
XX
DT 26-AUG-2004 (first entry)
XX
DE Rice ammonium transporter DNA with a T-DNA/GUS tag Seqid 12.
XX
KM rice; ammonium transporter; GUS; insertional mutagenesis;
KM beta-glucuronidase; biotic stress resistance; pesticide; herbicide;
KM plant; ds; hygromycin phosphotransferase; HGH; T-DNA; transfer-DNA;
KM chimeric.
XX
OS Oryza sativa.
OS Chimeric.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 1..96
FT /tag= a
FT /note= "T-DNA insert in rice line 1C-109-35"
XX
PN WO2004046357-A1.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-KR002461.
XX
PR 15-NOV-2002; 2002US-0427166P.
XX
PA (POSC-) POSCO.
PA (POST-) POSTECH FOUNDD.
XX
PI An G, Ryu C, Han J, Kang H, An K;
XX
XX WPI; 2004-449751/42.
XX
DR New organ preferential nucleic acids and polypeptides, useful in
XX producing rice plants with desired characteristics and which are
XX resistant to herbicide, plant pathogen, fungi, bacteria, virus, insect,
XX nematode, and stress.
XX
PS Disclosure; SEQ ID NO 12; 296bp; English.
XX
XX This invention relates to a novel method of identifying nucleic acid
XX molecules, or fragments thereof, that are expressed in an organ
XX preferential manner in rice. Specifically, it refers to producing rice
XX cell lines that carry tagged genes modified by T-DNA/GUS based
XX insertional mutagenesis, where the GUS portion of the insert is the
XX promoterless beta-glucuronidase reporter gene that can only be expressed
XX when it is inserted into an active gene. The present invention describes
XX generating transformed rice lines containing transfer-DNA (T-DNA)
XX insertions that also carry a gene encoding the selectable marker
XX hygromycin phosphotransferase (HPT). Accordingly, this method can be used
XX to produce rice plants with desirable characteristics including increased
XX grain yield and nutritional content, resistance to biotic stress,
XX pesticides, herbicides or insects, altered morphology or improved
XX characteristics referring to shape, taste or cooking quality of the
XX grain. This polynucleotide sequence represents the junction region that
XX links a genomic rice gene with a portion of the inserted T-DNA sequence,
XX given in an exemplification of the invention.
XX
XX Sequence 401 BP; 125 A; 89 C; 68 G; 119 T; 0 U; 0 Other;

Query Match 8.5%; Score 312; DB 12; Length 401;
Best Local Similarity 97.0%; Pred. No. 3.7e-18;
Matches 318; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2307 TGAGTTTTCTTGTCAGCAGCAGCAAGAAAAGCAGCAGTGAATAATATATTT 2366
DB 74 TGTGTTATTTAACTGTCTAAGCAGCCAGAAAGACACCTGAAAAAGTAGAATTTT 133
QY 2367 TTACAGCCTCCCATTTCCGTGCGTGACTTGTCAAAGTCTAATTTACGCGCGAGAGATGA 2426
DB 134 TTACAGCCTCCCATTTCCGTGCGTGACTTGTCAAAGTCTAATTTACGCGCGAGAGATGA 193
QY 2427 CTACAGTACTCCATATGCAATTTGCGATGACATCGAGGCACTGCTGATTCGCAAGGA 2486
DB 194 CTACAGTACTCCATATGCAATTTGCGATGACATCGAGGCACTGCTGATTCGCAAGGA 253
QY 2487 TCCGTGCTCTTATTTATGACACATGACACACCTACACCCCTTATCATTTATTTGTTT 2546
DB 254 TCCGTGCTCTTATTTATGACACATGACACACCTACACCCCTTATCATTTATTTGTTT 313
QY 2547 TTAGATTTGTGCGTAAATTAATACAGATTTCAATAGACATTAATGATTTTCTTTTCC 2606
DB 314 TTAGATTTGTGCGTAAATTAATACAGATTTCAATAGACATTAATGATTTTCTTTTCC 373
QY 2607 GTACACACACGAAATCTCAATTAATAT 2634
DB 374 GTACACACACGAAATCTCAATTAATAT 401

RESULT 11
AAL53989
ID AAL53989 standard; CDNA; 1961 BP.
XX
XX AAL53989;
XX
AC 18-FEB-2003 (first entry)
XX
DT
XX
DE cDNA encoding a soybean high affinity ammonium transporter protein #2.
XX
XX Herbicide; ammonium transporter protein; herbicide; transgenic plant;
XX KM soybean; gene; ss.
XX
XX Glycine max.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 214..1674
FT /tag= a
FT /product= "Soybean high affinity ammonium transporter
FT protein"
XX
XX US2002142390-A1.
XX
PN 03-OCT-2002.
XX
PD 28-DEC-2001; 2001US-00033109.
XX
PF 28-AUG-1998; 98US-0098248P.
XX
PR 27-AUG-1999; 99US-00384625.
XX
XX (ALIE/) ALLEN S M.
XX (RAFA/) RAFALSKI J A.
XX
PI Allen SM, Rafalski JA;
XX
XX WPI; 2003-102520/09.
XX
DR P-PSDB; AAO26537.
XX
XX Novel ammonium transporter polypeptide useful for identifying enzymatic
XX inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
XX transporter polypeptides.
XX
XX Claim 3; Page 21-22; 27pp; English.

The invention relates to a novel ammonium transporter protein comprising
90% homology based on the Clustal method compared to: a corn ammonium
transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
transporter polypeptide of 500 or 486 amino acids; a wheat ammonium

CC transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
CC transporter 497 amino acids fully defined in the specification. The
CC isolated polynucleotide is useful for selecting an isolated
CC polynucleotide that affects the level of expression of the ammonium
CC transporter polypeptide in a plant cell. The ammonium transporter protein
CC is useful for preparing antibodies which are useful for detecting the
CC transporter protein in situ in cells or in vitro in cell extracts, and as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that are useful as herbicides. The isolated polynucleotide is also useful
CC for creating transgenic plants in which the polynucleotide is present at
CC higher or lower levels than normal, and for designing and producing
CC primer pairs which are useful in amplification or primer extension
CC reactions. This polynucleotide sequence represents the cDNA encoding a
CC soybean high affinity ammonium transporter protein of the invention
XX
SQ Sequence 1961 BP; 490 A; 407 C; 472 G; 592 T; 0 U; 0 Other;
Query Match 7.9%; Score 289.6; DB 8; Length 1961;
Best Local Similarity 67.0%; Pred. No. 1.2e-34;
Matches 409; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
QY 353 CGTCGGTGGCGGAGCTGCTGAACAAGGGGAGCAACGCGTGGCAGCTGGTGGCGGAGCGC 412
DB 248 CGCGGGGACCCGAAATGGCTGAACAAGAGTGAACAACGATGGCAGCTAAACAGACGCCACC 307
QY 413 TGGTGGGCTGCGAGAGCGTCCGGCTTGGTGGTGGTGAACGGCGGCTGAAGAAGA 472
DB 308 TCGTGGCTCTTCAAGAGCATCCGGGTCTCGTGAATCCCTAAGCGCAGATGTGAAGAAA 367
QY 473 AGTGGGCGGAGAACTGGCGGCTTCAAGCGCTTACGCGCTTGGCGGCTGGATCGCT 532
DB 368 AATGGGAGGAACTGACCTTTCATGAGCTCTAAGCGCTTGGCGGCTTGAATATGTT 427
QY 533 GGGTCACTGGGGGCTACACATGCTCTTGGGGAGAACTCTCCGATCTGGGGAGAG 592
DB 428 GGGTGGCTGTGTATACGAAATGGCTTTGAGAGAACTTTCCCTTGGGGAGAG 487
QY 593 CGCGGGCGGCGTGAACAGAGGCTCTGCTGGCGCGCGCGGCTGCCGAGCGTCC 652
DB 488 GTGCTCCAGACATGAGCCAGAAAGTCTCTCAAGAAAGGCAATAGTATGAACCATCC 547
QY 653 ACTACCGCGCGGAGCGGAGGAGAGCGGGCGGAGCGGCTGACCGATGGCGA 712
DB 548 ACACCTTGAATAGGACATGTGAATACCTCTGAGAAACCTTTTACCTATGGCT 607
QY 713 CGGTGGTGAATCTCAAGTGGCTTGGCGCGCATACCTTCATCTGTCGCGGCTGCC 772
DB 608 CGCTGTGTATTTCCATTTCACTTTGCTGTATTACTTTATTTTGGTGGCTG 667
QY 773 TCGTGGCGGAGATGCTCTCGCTGTGAATCTTGTCCGCTGCTCACTTCT 832
DB 668 TCGTGGCGGAGATGATCAAGGCTTGAATGCTTGTGCTTGTGTATCTTTT 727
QY 833 CCAACCGCGGCGGCTTCTCTCTGCGGGCGGCGGCTCTCTTCACTGGGGGCTCA 892
DB 728 CCAACAGTGGGCGGCTTGAATGCTTGTGGGAGTGGCTTCTTCAACAAAGGGGCTTA 787
QY 893 TCGACTACTGGCGGCTGATCACTCACTCCGCGGAGTGGCGGCTTCAACCGCG 952
DB 788 TTGATATATTTGGCGGCTATGATACCTTTCTTGTGAATGCGGCTTCACTGCTG 847
QY 953 CTTACTGGGT 962
DB 848 CTTACTGGGT 857
RESULT 12
AEF16011
ID AEF16011 standard; cDNA; 1961 BP.
XX AEF16011;
AC AEF16011;
XX
DT 09-MAR-2006 (first entry)

XX
DE Glycine max ammonium transporter cDNA SeqID11.
XX
KW ammonium transfer; transgenic plant; nitrogen; cellular transport; gene;
XX ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 214..1674
FT /tag= a
FT /product= "Glycine max ammonium transporter"
XX
PN US2006010512-A1.
XX
PD 12-JAN-2006.
XX
PF 15-DEC-2004; 2004US-00012668.
XX
PR 28-DEC-2001; 2001US-00033109.
XX
PA (ALDE/) ALLEN S M.
XX PA (RAFA/) RAFALSKI J A.
XX
PI Allen SM, Rafalski JA;
XX
DR WPI, 2006-088761/09.
XX
DR P-PSDB; AEF16012.
XX
PT New isolated polynucleotide encoding a polypeptide having ammonium
PT transfer activity, useful for producing transgenic plants with increased
PT nitrogen content.
XX
PS Disclosure; SEQ ID NO 11; 29pp; English.
XX
SS This invention relates to a novel isolated polynucleotide encoding a
CC polypeptide having ammonium transfer activity. The polynucleotides are
CC useful for producing transgenic plants with increased nitrogen content.
CC The present sequence is a cDNA homologous to the sequence of the
CC invention which encodes an ammonium transporter.
XX
SQ Sequence 1961 BP; 490 A; 407 C; 472 G; 592 T; 0 U; 0 Other;
Query Match 7.9%; Score 289.6; DB 15; Length 1961;
Best Local Similarity 67.0%; Pred. No. 1.2e-34;
Matches 409; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
QY 353 CGTCGGTGGCGGAGCTGCTGAACAAGGGGAGCAACGCGTGGCAGCTGGTGGCGGAGCGC 412
DB 248 CGCGGGGACCCGAAATGGCTGAACAAGAGTGAACAACGATGGCAGCTAAACAGACGCCACC 307
QY 413 TGGTGGGCTGCGAGAGCGTCCGGCTTGGTGGTGGTGAACGGCGGCTGAAGAAGA 472
DB 308 TCGTGGCTCTTCAAGAGCATCCGGGTCTCGTGAATCCCTAAGCGCAGATGTGAAGAAA 367
QY 473 AGTGGGCGGAGAACTGGCGGCTTCAAGCGCTTACGCGCTTGGCGGCTGGATCGCT 532
DB 368 AATGGGAGGAACTGACCTTTCATGAGCTCTAAGCGCTTGGCGGCTTGAATATGTT 427
QY 533 GGGTCACTGGGGGCTACACATGCTCTTGGGGAGAACTCTCCGATCTGGGGAGAG 592
DB 428 GGGTGGCTGTGTATACGAAATGGCTTTGAGAGAACTTTCCCTTGGGGAGAG 487
QY 593 CGCGGGCGGCGTGAACAGAGGCTCTGCTGGCGCGCGCGGCTGCCGAGCGTCC 652
DB 488 GTGCTCCAGACATGAGCCAGAAAGTCTCAAGAAAGGCAATAGTATGAACCATCC 547
QY 653 ACTACCGCGCGGAGCGGAGGAGAGCGGGCGGAGCGGCTGATCCGATGGGAGCGA 712
DB 548 ACCACTTGAATAGGACATGTGAATACCTCTGAGAAACCTTTTACCTATGGCT 607
QY 713 CGGTGGTGAATCTCAAGTGGCTTGGCGCGCATACCTTCATCTGTCGCGGCTGCC 772

Db 608 CGCTGTGATTTCCAAATTCACCTTTTGTGCTATTACTCTATTATTGTGGCGCTCG 667
QY 773 TCCTCGGCGGCGATGAGCTTCTCGCTGGATGATCTTCCGCCGCTCGTCACTTCT 832
Db 668 TCCTTGGCCGAATGAAACATCAAGGCTTGATGCTTTGTGTGCTCTTTGTGATCTTT 727
QY 833 CCTACACCGTCGCGGCTTCTCCCTCTGGGGGCGGCGGCTTCTTCCACTGAGGGCGTCA 892
Db 728 CCTACACAGTCGCGGCTTTTAACTTTGGGGTGTGTGCTTTCTTACCAATGGGCGTTA 787
QY 893 TCGACTACTGCGCGGCTACGTCATCAGCTCTCCGCGGCAATCGCGGCTTACCGCG 952
Db 788 TTGATTATTCTGCGGCTATGTCATACACTTCTTCTGGAATCGCTGCTTCACTGCTG 847
QY 953 CTTACTGGGT 962
Db 848 CTTACTGGGT 857

RESULT 13

ACL28017
ID ACL28017 standard; cDNA; 977 BP.

XX ACL28017;
AC

DT 02-JUN-2005 (first entry)
XX

DE Rice abiotic stress responsive polynucleotide SEQ ID NO:1973.
XX

XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KM

XX agriculture.
XX

OS Oryza sativa.
XX

XX WO2003008540-A2.
PN

XX 30-JAN-2003.
PD

XX 21-JUN-2002; 2002WO-US019668.
XX

XX 22-JUN-2001; 2001US-0300112P.
PR

XX 24-AUG-2001; 2001US-0314662P.
PR

XX 26-SEP-2001; 2001US-0325277P.
PR

XX 21-NOV-2001; 2001US-0332132P.
XX

XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA

XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
PI Moughamer T, Provart N, Rieke D, Zhu T;
PI

XX WPI; 2003-248011/24.
DR

XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX

XX Claim 1; SEQ ID NO 1973; 89pp; English.
PS

XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX

SQL Sequence 977 BP; 131 A; 333 C; 330 G; 181 T; 0 U; 2 Other;

Query Match 7.6%; Score 279.6; DB 11; Length 977;
Best Local Similarity 78.3%; Pred. No. 3.5e-33;
Matches 349; Conservative 0; Mismatches 94; Indels 3; Gaps 1;

QY 2880 GCAGGGGATGTCAGAGGGGTGGGCGGCGCTGGTGTATGAGGGGATGCTCGCGGAGCATCCG 2939

Db 508 GCAGGCTGTGTGTCACACGCTGGGCGGCGCATGATGGGCATGTGTGGGCGAGCTTGGCG 567

QY 2940 TGTATACCAATGATGATCTTCCACAGCGCTTCCAAATCTTGTGACGCGGTGACACACC 2999

Db 568 TGGTCTCCATGATGATCTTCCACAGAGATCGGCGCTTCCAAAGGTGACACACC 627

QY 3000 CTCGGGCGTCTTCCACACCGCGGCTGCGCGGCGCTTCCGCGGCGCTTCCACCGGCGCTC 3059

Db 628 CTCGGGCGTCTTCCACACCGCGGCTGCGCGGCGCTTCCGCGGCGCTTCCACCGGCGCTC 687

QY 3060 TTGCGCGAGCCGACCCCTCTGCAACCTCTTCTCTCCGCTGCGCGACTTCCGCGGCGCTTTC 3119

Db 688 TTGCGCTTGTGCGGACCTTCAACGCGGCTTCCACACCGCATCTCCGCGGCGGCGGCTTTC 747

QY 3120 TAGGCGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3179

Db 748 TACGCGCGG---CGGATCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 804

QY 3180 GCGTGGAAAGTGTGTGTCACCTCCCTCACTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCTC 3239

Db 805 GTGTGAAAGTGTGTGTCACCTCCCTCACTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCTC 864

QY 3240 CGCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3299

Db 865 CGCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 924

QY 3300 GCGCTTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3325

Db 925 GCGCTATGGGAGAGCGGCGGAGGGA 950

RESULT 14

ADX3169
ID ADX3169 standard; cDNA; 796 BP.

XX ADX3169;
AC

XX 21-APR-2005 (first entry)
DT

XX Plant full length insert polynucleotide seqid 14489.
DE

XX plant protectant; plant growth regulant; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomanan production; lignin production; plant growth regulator;

XX yield; plant growth; plant development; seed oil; protein yield;
KM protein content; gene; ss.

XX Unidentified.
OS

XX US2004034888-A1.
PN

XX 19-FEB-2004.
PD

XX 28-APR-2003; 2003US-00425114.
PF

XX 06-MAY-1999; 99US-00304517.
PR

XX 05-NOV-2001; 2001US-00985678.
PR

XX (LIU/) LIU J.
PA

XX (ZHOU/) ZHOU Y.
PA

XX (KOVA/) KOVALIC D K.
PA

XX (SCRE/) SCREEN S E.
PA

Best Local Similarity 71.1%; Pred. No. 2.1e-28;
Matches 328; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY	2882	AGGGGTGATGCAGGGTGGCGGGCTGGTATGGGGTGTCGCCCGGACATCCGTG	294.1
Db	153	AGGCTGTGTGAAGGTGGGAGCACCATTGTATGGGAATTCTCTAGGTAGCATCCCTG	212
QY	2942	GTAACCACTGATGATCTCTCCACAAGCGCTCCAAAGATCTGCAAGCGCGTGCAGCACCTT	300.1
Db	213	GTACACTATGATGGTAGCTGCACAAAGMAATGGTCTTCATGCAAGAGATCGACGACACCTT	272
QY	3002	CGGGGTCTTTCACACCCACGGGGTGGCGGGCTCCTCGGGGAGCCTCTCACCGGCTCTT	306.1
Db	273	CGGGGTATTCACACCCCAATGGGGTGGCTGGGCTCTCGGGGCGCCACTACTGAGCTTTT	332
QY	3062	CGCCGAGCCACCCCTGTGCAA CTTCTTCTCCCGTTCGCGA CTCCGGGGCGCCTTTTA	312.1
Db	333	TGCTGAGGCTTCTCTGTGCMACTCTTCTCTGGCACTCCGGAGCTCBAAGGTGATTTTA	392
QY	3122	CGGCGGCGCGCGCGGCGGCCCA GTTGGGCAAGCATGCGCGGGCGCTCTTCTGTGTGCG	318.1
Db	393	TGGTGTGTATGTGTGATCACA GTTTGGGAACAGATTCCTGGCGCACTTTCGTATTTGG	452
QY	3182	CTGGAAGTGTGTCGTACACTCCCTCATGTGGCTGCGCAACCTCCCTGTCGGGCTCG	324.1
Db	453	CTGGAACATTGTATCACTTTCATATCTGTGTTTATTGGCCTAGTCTGCCCCCTCG	512
QY	3242	CATGCCCGACACAAAGCTCGAAGTGGCGACGACGCGCTCCA CGGCGAGAAGGCTTAAGC	330.1
Db	513	AATTCCTGATGCACAGCTGCTTATTCGGGGATGATCTGTAACTGGTGAAGAGCGTATGCG	572
QY	3302	GCTCTGGGGCAGCGCGGAGATGTACAGATCAACCAAGACG	334.2
Db	573	TATATGGGCAGAAAGCGAGCTCAAGATGTAACTCCGCAAG	613

Search completed: July 23, 2006, 20:00:02
Job time : 2153 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2006, 20:00:17 ; Search time 16351 Seconds
(without alignments)
12575.095 Million cell updates/sec

Title: US-10-713-648a-29

Perfect score: 3677
Sequence: 1 aaataaataacataagca.....aagctccatatttcccaaa 3677

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643.6	17.5	700	5	CT146333 CT146333
2	642.6	17.5	700	5	CT135879 CT135879
3	631	17.2	639	5	CK077340 CK077340
4	630.2	17.1	647	13	CT1795215 OR CBA000
5	604	16.4	650	5	CT138721 CT138721
6	557.8	15.2	599	5	CT146832 CT146832
7	556.4	15.1	650	5	CT145244 CT145244
8	554	15.1	600	5	CT127500 CT127500
9	551.8	15.0	639	5	CT1277861 CT1277861
10	535.6	14.6	581	5	CT142521 CT142521
11	531.4	14.5	589	4	CB678450 OSJNE16H
12	528	14.4	550	4	CT179219 CT179219
13	524.2	14.3	772	13	CZ885367 CZ885367
14	498	13.5	828	12	CC938910 ZMABD023
15	497.8	13.5	685	14	DX307908 OR ABA021
16	496	13.5	534	5	CT134465 CT134465
17	493	13.4	877	8	CO460978 MZCCL1503
18	487	13.2	855	8	CN126881 RHOH1_19
19	483	13.1	550	5	CT149540 CT149540

20	482.2	13.1	737	9	CX611918 CX611918
21	482	13.1	924	7	BF065831 BF065831
22	477.8	12.9	590	10	CW595602 CW595602
23	473.2	12.9	784	10	DV542942 DV542942
24	467.6	12.7	500	5	CT179182 CT179182
25	467.4	12.7	597	14	DX201805 DX201805
26	461.2	12.5	570	13	DUI61153 DUI61153
27	454	12.3	500	5	CT179514 CT179514
28	453	12.3	1497	13	CI960276 CI960276
29	451.8	12.3	877	13	CW004599 CW004599
30	447.8	12.2	882	12	CC427168 CC427168
31	444.6	12.1	647	10	DY347869 DY347869
32	439.8	12.0	673	4	CA141237 CA141237
33	423.8	11.5	800	14	DUI59289 DUI59289
34	422.4	11.5	471	5	CI355059 CI355059
35	420	11.4	707	13	CW168467 CW168467
36	419	11.4	770	10	DV522315 DV522315
37	418.8	11.4	734	13	CW405591 CW405591
38	411	11.2	640	4	CA191252 CA191252
39	405.6	11.0	450	5	CT177804 CT177804
40	404.4	11.0	964	10	DV856565 DV856565
41	403.8	11.0	679	12	CG470974 CG470974
42	400.6	10.9	685	10	DR790051 DR790051
43	399.4	10.9	447	5	CI345151 CI345151
44	398.6	10.8	742	12	CC607787 CC607787
45	394	10.7	708	12	CL151156 CL151156

ALIGNMENTS

RESULT 1
LOCUS CT146333
DEFINITION CT146333 Oryza sativa (japonica cultivar-group) mixed shoot
(Normalized Library) Oryza sativa (japonica cultivar-group) cDNA
clone 028-W081R-G03 3', mRNA sequence.
ACCESSION CT146333
VERSION CT146333.1 GI:86503700
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 700)
Kikuchi, S.
Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice
Unpublished (2006)
Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA Project
URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
Yamamoto, M. and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Natikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S.,
Yoshimura, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,

Akimura,T., Atakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Heshizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Iida,U., Imanura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koyama,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Otsu,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takeku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES

source

1..700
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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ORIGIN

Query Match 17.5%; Score 643.6; DB 5; Length 700;
Best Local Similarity 97.6%; Pred. No. 5,2e-116;
Matches 687; Conservative 0; Mismatches 9; Indels 8; Gaps 3;

OY 2958 CTCACACAGCGCTCCAGATCTCGACGCGCGTGCAGACACCTCGGCGTCTTCCACACC 3017
DB 1 CTCACACAGCGCTCCAGATCTCGACGCGCGTGCAGACACCTCGGCGTCTTCCACACC 60
OY 3018 CACGGCGTGGCGGCGCTCTCGGCGGCGCTCCACACCGGCTCTTCCGCGGACCCACCTC 3077
DB 61 CACGGCGTGGCGGCGCTCTCGGCGGCGCTCCACACCGGCTCTTCCGCGGACCCACCTC 120
OY 3078 TCACAACCTCTCTCCCGCTCGCGACCTCCGCGGCGCTTCTCAACGCGCGCGCGCGC 3137
DB 121 TCACAACCTCTCTCCCGCTCGCGACCTCCGCGGCGCTTCTCAACGCGCGCGCGCGC 180
OY 3138 GCCCAGTTGGCAGACAGATCGCGGCGGCTCTTCTCGTGGCTCGGAACGTCGTGTC 3197
DB 181 GCCCAGTTGGCAGACAGATCGCGGCGGCTCTTCTCGTGGCTCGGAACGTCGTGTC 240
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DB 241 ACCTCCCTATCGCTCGCGACATCACTCTCTCGCGCTCCGCGGACCGCGACGACG 300
OY 3258 CTCGAGTTCGGCGACACGCGCTCCACGCGCGAGAGAGGCTTACGCGCTCTGCGGCGACGCGC 3317
DB 301 CTCGAGTTCGGCGACACGCGCTCCACGCGCGAGAGAGGCTTACGCGCTCTGCGGCGACGCGC 360
OY 3318 GAGATGATAGAGTTCACCAAGCAGCGGCTCGACGCGCGGCTGCGCGCTCGTGTATGA 3377
DB 361 GAGATGATAGAGTTCACCAAGCAGCGGCTCGACGCGCGGCTGCGCGCTCGTGTATGA 420
OY 3378 TCGATCACATTAATGATGATGTCGACCTGATGAAGAACTCAAGAAATTCATACAC 3437
DB 421 TCGATGAC---ATTCATGATGTCGACCTGATGAAGAACTCAAGAAATTCATACAC 476
OY 3438 AGAAATTAATACGATGTTGCTTCTACTCGTTAATTAAGAAATCTAATGTTCAAGTT 3497
DB 477 AGAAATTAATACGATGTTGCTTCTACTCGTTAATTAAGAAATCTAATGTTCAAGTT 536
OY 3498 TACGATTAATTAACAGCGCGCGTGTGAG---TTAGCAATTCGACCTTTCGACATT- CAGG 3553
DB 537 TACGATTAATTAACAGCGCGCGTGTGAGTTTTCAGTATTCGACCTTTCGACATT- CAGG 596
OY 3554 GGAGTCCGGTTCGATTTTGTAGTTGTAAGAAATGAAATGATGATGTTTGTATCCTTA 3613
DB 597 GGAGTCCGGTTCGATTTTGTAGTTGTAAGAAATGAAATGATGATGTTTGTATCCTTA 656
OY 3614 CTGATCTGAATGAACACAGTGAATATTAATTTTGTAAAT 3657

DB 657 CTGATCTGAATGAACACAGTGAATATTTGTTAAT 700

RESULT 2
C1135879
LOCUS
DEFINITION
C1135879 Oryza sativa (japonica cultivar-group) mixed callus
(Normalized Library) Oryza sativa (japonica cultivar-group) cDNA
clone 027-M018R-A04 3', mRNA sequence.

ACCESSION
C1135879
VERSION
C1135879.1 GI:86493246

KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
clade; Ehrhartoideae; Oryzoae; Oryza.

REFERENCE
AUTHORS
TITLE
Kikuchi,S.
Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice

JOURNAL

Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agricultural Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007

Email: skikuchi@niae.affrc.go.jp
This EST clone is one of 780K ESTs of Rice full length cDNA Project
URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi,S., Satoh,K., Nigata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otsu,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Maeda,H., Miura,J., Mizuno,K., Nakikawa,R., Nikiura,T., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Atakawa,K., Akimura,T., Atakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Iida,U., Imanura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Otsu,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takeku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES

source

1..700
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="027-M018R-A04"
/tissue_type="mixed callus (Normalized Library)"
/clone_lib="Oryza sativa (japonica cultivar-group) mixed callus (Normalized Library)"

ORIGIN

Query Match 17.5%; Score 642.6; DB 5; Length 700;
Best Local Similarity 97.6%; Pred. No. 8,2e-116;
Matches 686; Conservative 0; Mismatches 9; Indels 8; Gaps 3;

Accession	Version	Keywords	Source	Organism	Reference	Authors	Title
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Db	1						
QY	3017						
Db	61						
QY	3077						
Db	121						
QY	3137						
Db	181						
QY	3197						
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Db	301						
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QY	3377						
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QY	3497						
Db	537						
QY	3554						
Db	597						
QY	3614						
Db	657						
RESULT 3							
LOCUS	CK077340						
DEFINITION	852633xrcen_27250.y1	Oryza sativa cv. LTP9	booting whole plant	CDNA			
ACCESSION	CK077340						
VERSION	CK077340.1	GI:58688653					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							

JOURNAL	PLOS Biol.	3 (2), e38	(2005)
PUBMED	15685292		
COMMENT	Contact: Yan Zhou Bioinformatics Department Hangzhou Genomics Institute No.51 ZhiJiang Road, Hangzhou 310008, China Tel.: 86-571-56805886 Fax: 86-571-56805884 Email: zhouyan@genomics.org.cn Seq primer: M13 Forward High quality sequence stop: 639 POLYA=No.		
FEATURES	location/Qualifiers		
SOURCE	1..639 /organism="Oryza sativa (indica cultivar-group)" /mol_type="mRNA" /cultivar="LYP9" /db_xref="taxon:39946" /tissue_type="whole plant" /dev_stage="bootling" /clone_lib="Oryza sativa cv. LYP9 bootling whole plant cdna library"		
ORIGIN			
Query March	17.2%; Score 631; DB 5; Length 639;		
Best Local Similarity	100.0%; Pred. No. 1.6e-113; Indels 0; Gaps 0;		
Matches 631; Conservative 0; Mismatches 0;			
Oy	271 AGCTTAGTGTGTTTGATCAGCCACGAMAGTGTGTGTGGCGACGGTGGTCGCCGCTG	330	
Db	9 AGCTTAGTGTGTGTGATCATCGACGACGAAGTGTGTGTGGCGACGGTGGTCGCCGCTG	68	
Oy	331 GCCTAACGAGGAAACAAGTCGGCGTCGGTGGCGCACTGGCTGAACAAAGGGGAAACAACGC	390	
Db	69 GCCTAACGAGGAAACAAGTCGGCGTCGGTGGCGCACTGGCTGAACAAAGGGGAAACAACGC	128	
Oy	391 TGGAGCTGTGTGGGGGAGCGCTGTGGGGCTGAGAAGCGTGGCGGCTTGTGGTGTCTG	450	
Db	129 TGGAGCTGTGTGGGGGAGCGCTGTGGGGCTGAGAAGCGTGGCGGCTTGTGGTGTCTG	188	
Oy	451 TAGCGCGCGCTGTGAAGAGAGAGTGGCGGTGAACCTCGCGTTTCATGCGCTTACGCC	510	
Db	189 TAGCGCGCGCTGTGAAGAGAGAGTGGCGGTGAACCTCGCGTTTCATGCGCTTACGCC	248	
Oy	511 TTGCGCGCGCTGTGATCTGCTGGCTCACCTGGGCGTACAAATGTGCTTGGGGAGAG	570	
Db	249 TTGCGCGCGCTGTGATCTGCTGGCTCACCTGGGCGTACAAATGTGCTTGGGGAGAG	308	
Oy	571 CTCTCTCCCGATCTGGGGGAGAGCGCGCGCGCGTGAACGAGGGCTCTCGTCGCGCGC	630	
Db	309 CTCTCTCCCGATCTGGGGGAGAGCGCGCGCGCGTGAACGAGGGCTCTCTGTGCGCGC	368	
Oy	631 GCCGCGCTGCGCGGACCGTCCACTTACCAGCCGACGACGCGACGTGAGACCGCGCGGTG	690	
Db	369 GCCGCGCTGCGCGGACCGTCCACTTACCAGCCGCGCGACGACGCGACGCGCGGTG	428	
Oy	691 GAGCGCTGTACCCGATGGACGAGCGGTGTATTCTTCAATGCGGTGTGGCGCATCAC	750	
Db	429 GAGCGCTGTACCCGATGGACGAGCGGTGTATTCTTCAATGCGGTGTGGCGCATCAC	488	
Oy	751 CTCATCTCTGTGCGCGGCTCCCTCTCGCGCGGATGAGCTTCTCGCGCTGATGATCTTC	810	
Db	489 CTCATCTCTGTGCGCGGCTCCCTCTCGCGCGGATGAGCTTCTCGCGCTGATGATCTTC	548	
Oy	811 GTCCGCGCTGTAGCTCACTTCTCTCTAACAAGTGGCGCTTCTCTCTGTGGGCGCGCGC	870	
Db	549 GTCCGCGCTGTAGCTCACTTCTCTCTAACAAGTGGCGCTTCTCTCTGTGGGCGCGCGC	608	
Oy	871 TTCCTTTCACACTGGGCGCTATGACTACT 901		
Db	609 TTCCTTTCACACTGGGCGCTATGACTACT 639		

RESULT 4	CL795215	647 bp	DNA	linear	GSS 06-AUG-2004
LOCUS	CL795215				
DEFINITION	CL795215				
ACCESSION	CL795215				
VERSION	CL795215.1	GI:51017231			
KEYWORDS	GSS.				
SOURCE	Oryza rufipogon				
ORGANISM	Oryza rufipogon				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Euharoidae; Oryzaceae; Oryza.				
AUTHORS	Kim,H., Yu,Y., Walsoski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jettly,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.				
TITLE	OMAP project				
JOURNAL	Unpublished (2004)				
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: rwing@genome.arizona.edu PCR Primers FORWARD: TAA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA Plate: 0004 row: P column: 07 Seq primer: CAC TCA TTA GGC ACC CCA Clas: BAC ends.				
FEATURES	Location/Qualifiers				
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	/tissue_type="Young leaves"				
	/dev_stage="2 week old seedlings"				
	/lab_host="DH10B T1 phage resistant"				
	/clone_1b="OR_CBA"				
	/note="Vector: pAG1BAC1, Site_1: HindIII, Site_2: HindIII dir treated 36 hrs before harvest"				
ORIGIN					
Query Match	17.1%; Score 630.2; DB 13; Length 647;				
Best Local Similarity	99.4%; Pred. No. 2.3e-113;				
Matches	643; Conservative 0; Mismatches 3; Indels 1; Gaps 1				
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1	AGTGTGTGTGAATCAGCGACGCAAGATGTCGTCTCGCGGACGCTGTGCGCGTGA 60				
336	CCAGGGGAACAGTGGCGCTCGGTGGCGGACCTGGCTGAAACAAGGGGACAAACGCTGGCA 395				
61	CCAGGGGAACAGTGGCGCTCGGTGGCGGACCTGGCTGAAACAAGGGGACAAACGCTGGCA 120				
396	GCTGTGGCGCGGACGCTGTGGGCGTGAAGACGTCGCGGCGCTTGTGTGCTGTGACGG 455				
121	GCTGTGGCGCGGACGCTGTGGGCGTGAAGACGTCGCGGCGCTTGTGTGCTGTGACGG 180				
456	CGGCGTGTGAAGAAAGATGGGCGGTGAACCTCGGCGTTCAATGCGGCTTACGCGCTTGGC 515				
181	CGGCGTGTGAAGAAAGATGGGCGGTGAACCTCGGCGTTCAATGCGGCTTACGCGCTTGGC 240				
516	CGCGTGTGTGATCTGTGCTGCTCACTTGGGCGTGAACAACATGTCTGGGGAGAAAGTCTCT 575				
241	CGCGTGTGTGATCTGTGCTGCTCACTTGGGCGTGAACAACATGTCTGGGGAGAAAGTCTCT 300				
576	CCCGATCTGGGGGAAAGGCGGCGCGGCGCTGGACCAAGGCGCTCTCGTGTGGCGGCGCGC 635				
301	CCCGATCTGGGGGAAAGGCGGCGCGGCGCTGGACCAAGGCGCTCTCTGTGTGGCGGCGCGC 360				

OY	636	GCTGCCGGCCACCGTCCACTACCGCGCCGACGAGCGTGTGAGACACGGCGCGGTGAGACC	695
Db	361	GCTCCCGGCGACGGTTCACCTACCGCGCCGACGAGCGTGTGAGACACGGCGCGGTGAGACC	420
OY	696	GCTGTACCCGATGCGACGAGTGTGTCTTCACAGTGGCTGTTCGCCGCCATCATCCCTCAT	755
Db	421	GCTGTACCCGATGCGACGAGTGTGTCTTCACAGTGGCTGTTCGCCGCCATCATCCCTCAT	480
OY	756	CTTCGTGCGCGGCTCCCTCCTCGGCGGCATGAGCTTCTCGCTCGATGATCTTCGTGCC	815
Db	481	CCTGTGCGCGGCTCCCTCCTCGGCGGCATGAGCTTCTCGCTCGATGATCTTCGTGCC	540
OY	816	GCTGTGCGTCACTTCTCCTACACCGTCCGCGGCTTCTCCCTCTGGGCGCGGCTTCCT	875
Db	541	GCTGTGCGTCACTTCTCCTACACCGTCCGCGGCTTCTCCCTCTGGGCGCGGCTTCCT	600
OY	876	CTTCGACTGGGGCGCTCA-TCGACTACTGCGGCGGCTACGTCATCCAC	921
Db	601	CTTCGACTGGGGCGCTCACTGACTACGCGGCGGCTACGTCATCCAC	647
RESULT 5			
C1138721			
LOCUS			
DEFINITION	C1138721 Oryza sativa (japonica cultivar-group) mixed callus (Normalised library) Oryza sativa (japonica cultivar-group) CDNA clone 027-M076R-H04 3', mRNA sequence.		
ACCESSION	C1138721		
VERSION	C1138721.1	GI:86496088	
KEYWORDS	EST.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Euhartotidae; Oryzaceae; Oryza.		
AUTHORS	1 (bases 1 to 650)		
TITLE	Kikuchi, S.		
JOURNAL	Collection and mapping of over 30,000 transcription units by the rice full-length CDNA project from japonica rice		
COMMENT	Unpublished (2006)		
	Contact: Shoshi Kikuchi		
	Department of Molecular Genetics, Head of Laboratory of Gene Expression		
	National Institute of Agrobiological Sciences		
	2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan		
	Tel.: 81-29-838-7007		
	Fax: 81-29-838-7007		
	Email: skikuchi@nias.affrc.go.jp		
	This EST clone is one of 780K ESTs of Rice full length CDNA project URL: http://cdna01.dna.affrc.go.jp/cDNA/NIMS Rice Full-length CDNA Project Team: Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nemiki, T., Ohneda, E., Yahagi, M., Suzuki, K., Li, C., Ohnuki, K., Shishiki, T., Yamamoto, M., and Nakahama, Y.		
	FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusunegi, T., Lu, M., Masuda, H., Miura, J., Miuno, K., Nariwaka, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tanudaa, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.		
	Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, S., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanzaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hitamoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imochi, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Seto, K., Shibata, K., Shinagawa, A., Shiraki, T.,		

Sogabe, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers

FEATURES

Source
1. 650
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/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="027-M076R-H04"
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callus (Normalized Library)"

ORIGIN

Query Match 16.4%; Score 604; DB 5; Length 650;
Best Local Similarity 97.4%; Pred. No. 3.3e-108;
Matches 637; Conservative 0; Mismatches 10; Indels 7; Gaps 2;
2984 GCGCGTCGACGACACCTTCGCGGCTTTCACACCGCGCGCTTCCTCGCGCG 3043
1 GCGCGTCGACGACACCTTCGCGGCTTTCACACCGCGCGCTTCCTCGCGCG 60
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61 CCTCTCAACGGGCTTCCTCGCGGACCCCTTCGCAACCTTCCTCCCGCTCGCGCA 120
3104 CTCCCGGCGGCGCTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3163
121 CTCCCGGCGGCGCTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
3164 CGGCGCTTCCTTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3223
181 TGCGCGCTTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 240
3224 CCTCTTCGCA 3283
241 CCTCTTCGCA 300
3284 CGGCGGAGAGCGCTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3343
301 CGGCGGAGAGCGCTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
3344 CTCCGACCGCGCGCTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3403
361 CTCCGACCGCGCGCTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 416
3404 CACCTGATGAAAACCTCAAGAAATTCATACACAGAAATTAATACGCTTTC 3463
417 CACCTGATGAAAACCTCAAGAAATTCATACACAGAAATTAATACGCTTTC 476
3464 TACTGCTTAATGAAAATTCATGTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 3523
477 TACTGCTTAATGAAAATTCATGTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 536
3524 GAG--TTAGGACATTCGACCTTCGACATTCAGGAGAGTCGCTTCTGTAATTT 3580
537 GAGTTTTCGATTCGACCTTCGACATTCAGGAGAGTCGCTTCTGTAATTT 596
3581 TTGTAATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 3634
597 TTGTAATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 650

RESULT 6
C1146832 599 bp mRNA linear EST 05-FEB-2006
LOCUS C1146832 Oryza sativa (japonica cultivar-group) mixed shoot
DEFINITION (Normalized Library) Oryza sativa (japonica cultivar-group) cDNA
clone 028-M090R-B07 3', mRNA sequence.
ACCESSION C1146832
VERSION C1146832.1 GI:86504199
KEYWORDS EST.

SOURCE

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BIP
clade; Eriocaulaceae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 599)

AUTHORS

Kikuchi, S.

TITLE

Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice

JOURNAL

Unpublished (2006)

COMMENT

Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agricultural Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA project
URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-Length_cDNA_Project_Team_Kikuchi_S_Sato_K_Nagata_T_Kawagashira_N_Doi_K_Kishimoto_N_Yazaki_U_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ohmeda_E_Yahagi_M_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_Yamamoto_M_and_Nakahama_Y_FAIR_Genome_Sequencing_and_Analysis_Group_Oromo_Y_Iida_Y_Fujimura_T_Ikeda_R_Ishibiki_U_Kawamata_M_Kobayashi_M_Kodama_T_Kuroaki_T_Kusumegi_T_Lu_M_Masuda_H_Miura_J_Mizuno_K_Narikawa_R_Nikura_J_Oka_M_Ryu_R_Sugano_S_Sugiyama_A_Suzuki_Y_Tsunoda_Y_Ueda_M_Xie_Q_Yokomizo_S_Yoshimura_A_Matsubara_K_and_Murakami_K_Genome_Exploration_Research_Group_in_Riken_Genomic_Sciences_Center_and_Genome_Science_Laboratory_in_Riken_Adaichi_U_Aizawa_K_Akimura_T_Arakawa_T_Carninci_P_Fukuda_S_Hanagaki_T_Hara_A_Hashizume_W_Hayashida_K_Hayatsu_N_Hiramoto_K_Hirooka_T_Hori_F_Iida_J_Imanishi_K_Iimoto_K_Ishii_Y_Itoh_M_Kagawa_I_Kanagawa_S_Katoh_H_Kawai_U_Kishikawa_Hirozane_T_Kojima_Y_Kondo_S_Kono_H_Konda_M_Koya_S_Kurimura_C_Matsuyama_T_Miyazaki_A_Murata_M_Nakamura_M_Nishi_K_Nomura_K_Nunashi_N_Ohno_M_Osato_N_Ota_Y_Saitoh_H_Sakai_C_Sakai_K_Sakazume_N_Sano_H_Sasaki_D_Sato_K_Shibata_K_Shingawa_A_Shiraki_T_Sogabe_Y_Tagami_M_Tagami-Takeda_Y_Tagawa_A_Takahashi_F_Takaku-Akahira_S_Tanaka_T_Tomaru_A_Toya_T_Waki_K_Yasunishi_A_and_Hayashizaki_Y_Location/Qualifiers

FEATURES

Source

1. 599
/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="Oryza sativa (japonica cultivar-group) mixed
shoot (Normalized Library)"

ORIGIN

Query Match 15.2%; Score 557.8; DB 5; Length 599;
Best Local Similarity 97.7%; Pred. No. 4.2e-99;
Matches 589; Conservative 0; Mismatches 7; Indels 7; Gaps 2;
2996 CACCTTCGCGGCTTCGACACCGCGCGCTTCGCGGCGCGCGCGCGCGCGCG 3055
1 CACCTTCGCGGCTTCGACACCGCGCGCTTCGCGGCGCGCGCGCGCGCGCGCG 60
3056 CCTCTTCGCGGCG 3115
61 CCTCTTCGCGGCG 120
3116 CTCTTCGCGGCG 3175
121 CTCTTCGCGGCG 180

RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
3176	C1145244	C1145244 Oryza sativa (japonica cultivar-group) mixed shoot (Normalized library) Oryza sativa (japonica cultivar-group) cDNA clone 028-M066R-E06 3', mRNA sequence.	C1145244				Oryza sativa (japonica cultivar-group)	EST.				
Db							Oryza sativa (japonica cultivar-group)					
3181							Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrharioideae; Oryzeae; Oryza.					
3236							1 (bases 1 to 650)					
3236							Kikuchi, S.					
3241							Collection and mapping of over 30,000 transcription units by the rice full-length cDNA project from japonica rice					
3296							Unpublished (2006)					
3301							Contact: Shoichi Kikuchi					
3356							Department of Molecular Genetics, Head of Laboratory of Gene Expression					
3416							National Institute of Agricultural Sciences					
417							2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan					
477							Tel: 81-29-838-7007					
3476							Fax: 81-29-838-7007					
477							Email: skikuchi@nias.affrc.go.jp					
3533							This EST clone is one of 780k ESTs of Rice full length cDNA Project					
537							URL: http://cdna01.dna.affrc.go.jp/cDNA/					
3593							NIRS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,					
597							Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,					
599							Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,					
							Onoda, E., Yabagi, W., Suzuki, K., Li, C., Oheguchi, K., Shieniki, T.,					
							Yanamoto, M., and Nakahama, Y.					
							PAIS Genome Sequencing & Analysis Group: Otsomo, Y., Iida, Y.,					
							Fujimura, T., Ikeda, T., Ishibiki, J., Kawamata, M., Kobayashi, M.,					
							Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J.,					
							Mizuno, K., Nariikawa, R., Nikura, Y., Oka, M., Ryu, R., Sugano, S.,					
							Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,					
							Yoshimura, A., Matsubara, K., and Murakami, K.					

Db	Query Match	Best Local Similarity	Matches	574; Conservative	0; Mismatches	6; Indels	4; Gaps	1; Gaps
OY	2879	TGCAGGGGTGTGTGAGAGGGGTGGGGGGGGGCGTGGTATGGGGGGTGTGCGCGGACATATCCC	2938	15.1%; Score 556.4; DB 5; Length 650;				
Db	64	TGCAGGGGTGTGTGAGAGGGGTGGGGGGGGTGGTATGGGGGGTGTGCGCGGACATATCCC	123	98.3%; Pred. No. 8.1e-99;				
OY	2939	GTGGTACACCATGATGATCTTCCACCAAGCGCTCCAGATCCTGACGGCGGTGACGAC	2998					
Db	124	GTGGTACACCATGATGATCTTCCACCAAGCGCTCCAGATCCTGACGGCGGTGACGAC	183					
OY	2999	CCTGGGGCTCTTCAACACCCACGGCGTGGCGGCTCTTGGCGGGCTTCTTCAACGGGCT	3058					
Db	184	CCTGGGGCTCTTCAACACCCACGGCGTGGCGGCTCTTGGCGGGCTTCTTCAACGGGCT	243					
OY	3059	CTTGGCGGAGCGCAACCTCTGCAACCTCTTCCCTCCCGCTGGCGGACCTCCGGGGCGGCTT	3118					
Db	244	CTTGGCGGAGCGCAACCTCTGCAACCTCTTCCCTCCCGCTGGCGGACCTCCGGGGCGGCTT	303					
OY	3119	CTACGGCGGCGCCGCGCGGCGCCAGTTCCGACAGCATCGCCGCGGCGCTTCTGTCGT	3178					
Db	304	CTACGGCGGCGCCGCGCGGCGCCAGTTCCGACAGCATCGCCGCGGCGCTTCTGTCGT	363					
OY	3179	CGCCTGGAAGTGTGTCACCTTCCCTCATCTGCTCGCATCAACTCTCTGTCGGCT	3238					
Db	364	CGCCTGGAAGTGTGTCACCTTCCCTCATCTGCTCGCATCAACTCTCTGTCGGCT	423					
OY	3239	CCGATGCGCGACGACAAGCTCGAGGTCCGGGACGACGCGCTCCACGGCGGAGGAGCTTA	3298					
Db	424	CCGATGCGCGACGACAAGCTCGAGGTCCGGGACGACGCGCTCCACGGCGGAGGAGCTTA	483					
OY	3299	CGCGCTCTGGGGGACGCGCGAGATGTAAGAGTCACCAAGACGCGCTCCGACGCGCGCT	3358					
Db	484	CGCGCTCTGGGGGACGCGCGAGATGTAAGAGTCACCAAGACGCGCTCCGACGCGCGCT	543					
OY	3359	TGCCCCGCTGTCGTATGATGATGATCACTTAATTCATGTCGTGTCACCTGATATAAAC	3418					
Db	544	TGCCCCGCTGTCGTATGATGATGATCACTTAATTCATGTCGTGTCACCTGATATAAAC	599					
OY	3419	TCAAGAAATTCATACACACAGAAATTAATTAATCTAGTGTGGCTT	3462					
Db	600	TCAAGAAATTCATACACACAGAAATTAATTAATCTAGTGTGGCTT	643					

Yamamoto, M. and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J.,
Mizuno, K., Narikawa, R., Nishikawa, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Otsu, N.,
Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takahara, A., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers

FEATURES
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1. 639
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/mol_type="rRNA"
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/db_xref="taxon:39947"
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shoot (Normalized Library)"

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Query Match 15.0%; Score 551.8; DB 5; Length 639;
Best Local Similarity 98.0%; Pred. No. 6.5e-98;
Matches 581; Conservative 0; Mismatches 7; Indels 5; Gaps 2;

2879 TGCAGGGGGTGTGCGAGGGGGTGGGGGGTGTGAGTGGGGGGTGTGGCGGAGAGATGCC 2938
51 TGCAGGGGGTGTGCGAGGGGGTGGGGGGTGTGAGTGGGGGGTGTGGCGGAGAGATGCC 110
2939 GTGTATACACATGATGATCTCTCCACAAAGCGCTCCAAAGATCTGACGCGCTGACGACAC 2998
111 GTGTATACACATGATGATCTCTCCACAAAGCGCTCCAAAGATCTGACGCGCTGACGACAC 170
2999 CCTGGCGCTTTTCACACCCCAAGCGCGCTGCGCGCTCTCTCGGGCGCTCTCTCAACGGCCT 3058
171 CCTGGCGCTTTTCACACCCCAAGCGCGCTGCGCGCTCTCTCGGGCGCTCTCTCAACGGCCT 230
3059 CTTGGCGCGCGCACCCCTGTGCAACTCTTCTCCCGCGCGCGACTCCCGGGGGCGCCTT 3118
231 CTTGGCGCGCGCACCCCTGTGCAACTCTTCTCTCCCGCGCGCGACTCCCGGGGGCGCCTT 290
3119 CTACGGCGCGCGCGCGCGCGCGCGCGCGAGTTGCGCAAGCATGCGCGCGCGCTCTTCTGCT 3178
291 CTACGGCGCGCGCGCGCGCGCGCGCGCGAGTTGCGCAAGCATGCGCGCGCGCTCTTCTGCT 350
3179 CGCCTGGAAGCTGTGTGATCACTCTCTCTCTCTGCTCTGCGCATCAACTCTTCTGCTCCGCT 3238
351 CGCCTGGAAGCTGTGTGATCACTCTCTCTCTCTGCTCTGCGCATCAACTCTTCTGCTCCGCT 410
3239 CGCGATGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCGCAAGCATGCGCGCGCGCTCTTCTGCT 3298
411 CGCGATGCGCGCGCGCGCGCGCGCGCGCGCGAGTGTGCGCAAGCATGCGCGCGCGCTCTTCTGCT 470
3299 CGCGCTCTGGGGGCGAGCGCGAGATGTATCGACGCTCAACGAACGCGCTCCGCGCGCGCT 3358
471 CGCGCTCTGGGGGCGAGCGCGAGATGTATCGACGCTCAACGAACGCGCTCCGCGCGCGCT 530
3359 TGGCCCGCTGCTGTGTATGATCATCAATTAATGATGTGCTGTGATCACTGATGAATCC 3418
531 TGGCCCGCTGCTGTGTATGATCATCAATTAATGATGTGCTGTGATCACTGATGAATCC 586

Ory 3419 T-CAGGAATTCATACACAGAAATTAATACTAGCTGGTCTTCTACTCGT 3470
Db 587 TCCAGGAATTCATACACAGAAATTAATACTAGCTGGTCTTCTACTCGT 639
RESULT 10
C1142521
LOCUS
DEFINITION
C1142521 Oryza sativa (japonica cultivar-group) mixed shoot
(Normalized Library-D05 3', mRNA sequence).
C1142521
VERSION
C1142521.1 GI:86499888
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartioideae; Oryzaceae; Oryza.
1 (bases 1 to 581)
REFERENCE
Kikuchi, S.
Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice
Unpublished (2006)
Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@niias.affrc.go.jp

This EST clone is one of 780k ESTs of Rice full length cDNA Project
URL: <http://cna01.dna.affrc.go.jp/cDNA/NIAS>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shieniki, T.,
Yamamoto, M. and Nakahama, Y.

FAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J.,
Mizuno, K., Narikawa, R., Nishikawa, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Otsu, N.,
Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takahara, A., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers

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1. 581
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="rRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="028-M029R-D05"
/cissue_type="mixed shoot (Normalized Library)"
/clone_lib="Oryza sativa (japonica cultivar-group) mixed
shoot (Normalized Library)"

ORIGIN
Query Match 14.6%; Score 535.6; DB 5; Length 581;
Best Local Similarity 98.0%; Pred. No. 1e-94;

Matches 575; Conservative 0; Mismatches 5; Indels 7; Gaps 3;

QY 2912 GATGGGGGTGCTCGCCGCGAGCATCCGCTGTAACATGATGATCTTCAACAGGCTC 2971
DB 1 GATGGGGGTGCTCGCCGCGAGCATCCGCTGTAACATGATGATCTTCAACAGGCTC 60

QY 2972 CAAGATCCGAGCGCGTGCAGACACCTCGCGCTTCCACACCCAGGGGTGCGCG 3031
DB 61 CAAGATCCGAGCGCGTGCAGACACCTCGCGCTTCCACACCCAGGGGTGCGCG 120

QY 3032 CCTCTCGGCGGCTCTCTCAACGCGCTCTTTCGCGAGCCACCTCTGCAACTCTTCT 3091
DB 121 CCTCTCGGCGGCTCTCTCAACGCGCTCTTTCGCGAGCCACCTCTGCAACTCTTCT 180

QY 3092 CCCCTGCGCACTCCCGGGGCGCTTCTTACGCGCGCGCGCGCGCCAGTTGCGCA 3151
DB 181 CCCCTGCGCACTCCCGGGGCGCTTCTTACGCGCGCGCGCGCGCCAGTTGCGCA 240

QY 3152 GAGATGCG -CGGCGGCTCTTCTGCTGCTGAGCAAGCTGCTGCACTCCCTCATCT 3210
DB 241 GAGATGCGCGCGGCTCTTCTGCTGCTGAGCAAGCTGCTGCACTCCCTCATCT 300

QY 3211 GCTCGGCACTCAACCTCTGCTGCTGCGCTGCGATGCGCGAGCAAGCTGAGTGGCG 3270
DB 301 GCTCGGCACTCAACCTCTGCTGCTGCGCTGCGATGCGCGAGCAAGCTGAGTGGCG 360

QY 3271 ACAGCGCGCTGCGAGCGCGAGGAGCTTACGCGCTTGGGGCGAGCGGAGTGTAGCAG 3330
DB 361 ACAGCGCGCTGCGAGCGCGAGGAGCTTACGCGCTTGGGGCGAGCGGAGTGTAGCAG 420

QY 3331 TCACCAAGACGCGCTTCCAGCGCGCGTGGCCCGCTGCTGATGATGATCACTTAA 3390
DB 421 TCACCAAGACGCGCTTCCAGCGCGCGTGGCCCGCTGCTGATGATGATCACTTAA 476

QY 3391 TTGCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3450
DB 477 TTGCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536

QY 3451 ACCTGTTTCTTCTACTCTGTTAATTATGAAATCTATGTTCAAGTTT 3497
DB 537 ACCTGTTTCTTCTACTCTGTTAATTATG--AATCTATGTTCAAGTTT 581

RESULT 11
CB678450 589 bp mRNA linear EST 09-APR-2003
LOCUS OSJNB16H13.f OSJNB Oryza sativa (japonica cultivar-group) cDNA
DEFINITION Clone OSJNB16H13 5', mRNA sequence.
ACCESSION CB678450
VERSION CB678450.1 GI:29682175
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
1 (bases 1 to 589)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stalberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wang,R.A.,
Soderlund,C., and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
1588683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers

FORWARD: gta aaa cga cgg cca gth
BACKWARD: gga aac agc tat gac cat g
Plate: 16 row: H column: 13
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers

FEATURES
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/cultiVar="Nipponbare"
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XhoI, 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN

Query Match 14.5%; Score 531.4; DB 4; Length 589;
Best Local Similarity 96.1%; Pred. No. 6.8e-94;
Matches 568; Conservative 0; Mismatches 16; Indels 7; Gaps 2;

QY 3066 GAGCCCAACCTCTGCAACCTCTTCCCTCCGCGCGAGCTCCGCGGCGCTTCTTACGCG 3125
DB 589 GAGCCCAACCTCTGCAACCTCTTCCCTCCGCGCGAGCTCCGCGGCGCTTCTTACGCG 530

QY 3126 GCGCGCGCGCGCGCGCGAGTTGGCAAGAGATGCGCGCGCGCTTCTGCTGCTGCG 3185
DB 529 GCGCGCGCGCGCGCGCGAGTTGGCAAGAGATGCGCGCGCGCTTCTGCTGCTGCG 470

QY 3186 AACGTGCTGATCACTCTCTCATCTGCTGCGCATCAACCTGCTGCTGCTGCGCGATG 3245
DB 469 AACGTGCTGATCACTCTCTCATCTGCTGCGCATCAACCTGCTGCTGCTGCGCGATG 410

QY 3246 CCCGACGACAGCTGAGGTCGCGAGCGAGCGCGCTGCAAGGAGGAGGCTTACGCGCTC 3305
DB 409 CCCGACGACAGCTGAGGTCGCGAGCGAGCGCGCTGCAAGGAGGAGGCTTACGCGCTC 350

QY 3306 TGGGGCGAGCGGAGATGTACAGCTCAACAGCAGCGCTCCGAGCGCGCGCTTGGCCCG 3365
DB 349 TGGGGCGAGCGGAGATGTACAGCTCAACAGCAGCGCTCCGAGCGCGCGCTTGGCCCG 290

QY 3366 GTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3425
DB 289 GTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 234

QY 3426 ATTCTATACACAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3485
DB 233 ATTCTATACACAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 174

QY 3486 ATGTTCAAGTTTAAAGTATTAACAAGCGCGGTGGAG--TTAGGATTTGACCTT 3542
DB 173 ATGTTCAAGTTTAAAGTATTAACAAGCGCGGTGGAGTTTAAAGTATTTGACCTT 114

QY 3543 GCAATTACAGGAGTCCGCTGCTGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3602
DB 113 GCAATTACAGGAGTCCGCTGCTGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 54

QY 3603 TTGTATCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3653
DB 53 TTGTATCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3

RESULT 12
C1179219 550 bp mRNA linear EST 06-FEB-2006
LOCUS C1179219 Oryza sativa (japonica cultivar-group) supermix Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 034-M062R-F07 3', mRNA
sequence.
ACCESSION C1179219
VERSION C1179219.1 GI:86539013
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eurycotyla, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bp
 clade; Eriophoroideae; Oryzoideae; Oryza.
 1 (bases 1 to 550)
REFERENCE
AUTHORS Kikuchi, S.
TITLE Collection and mapping of over 30,000 transcription units by the
 rice full-length cDNA project from japonica rice
 Unpublished (2006)
JOURNAL Contact: Shoshi Kikuchi
 Department of Molecular Genetics, Head of Laboratory of Gene
 Expression
 National Institute of Agricultural Sciences
 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: 81-29-838-7007
 Fax: 81-29-838-7007
 Email: skikuchi@ias.affrc.go.jp
 URL: http://cdna01.dna.affrc.go.jp/cdna/

This EST clone is one of 780k ESTs of Rice full length cDNA Project
 URL: http://cdna01.dna.affrc.go.jp/cdna/
NIMS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, U.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
 Yamamoto, M., and Nakahama, Y.
PAYS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Maeda, H., Mura, J.,
 Mizuno, K., Narikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S.,
 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
 and **Genome Science Laboratory in Riken:** Adachi, J., Aizawa, K.,
 Akimura, T., Aikawa, T., Carrin, P., Hayashida, K., Hayashida, K.,
 Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hayashida, K.,
 Hirooka, T., Hori, F., Iida, J., Imamura, K., Imoto, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
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 Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
 Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
 Takaku-Akhiba, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
 Yasunishi, A., and Hayashizaki, Y.
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 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
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 supermix"

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 Best Local Similarity 98.4%; Pred. No. 3.2e-93;
 Matches 545; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

2992 ATGATCTTCACAAAGGCTCTCAAGATCTCGACAGGCGTGCAGACACCTCGGCGCTTC
 Db 1 ATGATCTTCACAAAGGCTCTCAAGATCTCGACAGGCGTGCAGACACCTCGGCGCTTC 60
 3012 CACACCCACAGGCGTGCAGGCTCTCGGCGGCTCTTCACCGGCTCTTCGCGAGCC 3071
 Db 61 CACACCCACAGGCGTGCAGGCTCTCGGCGGCTCTTCACCGGCTCTTCGCGAGCC 120
 3072 ACCCTCTGCAACTCTCTCCCGTGCAGTCTCCCGGCGGCTCTTCGCGAGCC 3131
 Db 121 ACCCTCTGCAACTCTCTCCCGTGCAGTCTCCCGGCGGCTCTTCGCGAGCC 180

Qy 3132 GCGGCGCCCAAGTTGCGAGAGATCGCGGCGGCTCTTCGTCGCTCGACGTC 3191
 Db 161 GCGGCGCCCAAGTTGCGAGAGATCGCGGCGGCTCTTCGTCGCTCGACGTC 240
 Qy 3192 GTGTACCTCCCTGATGCTGCTCGCATCAACCTCTGTCGCTCGATGCCGAC 3251
 Db 241 GCGTCACCTCCCTGATGCTGCTCGCATCAACCTCTGTCGCTCGATGCCGAC 300
 Qy 3252 GACAGCTTCGAGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3311
 Db 301 GACAGCTTCGAGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 Qy 3312 GACGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3371
 Db 361 GACGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Qy 3372 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3431
 Db 421 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
 Qy 3432 ACACACAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3491
 Db 477 ACACACAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 536
 Qy 3492 AAGTTTACGTGA 3505
 Db 537 AAGTTTACGTGA 550

RESULT 13
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LOCUS 206.1.11970610.3.3763.077 Barley methylation filtered library
DEFINITION (Lifid: 206) Hordeum vulgare genomic, genomic survey sequence.
ACCESSION CZ885367
VERSION CZ885367.1 GI:75679853
KEYWORDS GSS.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
 Eurycotyla, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bp
 clade; Pooidae; Triticeae; Hordeum.
 1 (bases 1 to 772)
REFERENCE
AUTHORS Rabinowicz, P.D., Citek, R.W., Budiman, M.A., Nunberg, A., Bedell, J.A.,
 Lakey, N., O'Shaughnessy, A.L., Nascimben, L.U., McCombie, W.R. and
 Mattheisen, R.A.
 Differential methylation of genes and repeats in land plants
 Genome Res. 15 (10), 1431-1440 (2005)
 16204196

TITLE The Institute for Genomic Research
JOURNAL 9712 Medical Center Dr., Rockville, MD 20850, USA
PUBMED Tel: 301 795 7787
 Fax: 301 838 0208
 Email: pablo@igf.org
 Class: methylation filtered
 High quality sequence stop: 772.
FEATURES
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 1..772
 Location/Qualifiers
 /organism="Hordeum vulgare"
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 /db_xref="taxon:4513"
 /clone_1ib="Barley methylation filtered library (Lifid:
 206)"

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 Best Local Similarity 86.8%; Pred. No. 1.8e-92;
 Matches 577; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 306 GTGTGCGGAGAGT 365
 Db 672 GCGGCGCCAAAGT 613


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RESULT 15
LOCUS      DX307908                      685 bp    DNA          linear    GSS 20-JAN-2006
DEFINITION OR_Aba0219N14.r OR_Aba Oryza ridleyi genomic clone OR_Aba0219N14
3' genomic survey sequence.
ACCESSION  DX307908
VERSION    DX307908.1  GI:85584678
KEYWORDS   GSS.
SOURCE     Oryza ridleyi
ORGANISM   Oryza ridleyi
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 685)
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
            OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
            Unpublished (2005)
TITLE      JOURNAL
COMMENT    Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: twing@genome.arizona.edu
            Plate: 0219  Row: N  Column: 14
            Class: BAC ends.
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                /db_xref="taxon:83308"
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Query Match      13..5%; Score 497.8; DB 14; Length 685;
Best Local Similarity 91.5%; Pred. No. 2..9e-87;
Matches 561; Conservative 0; Mismatches 47; Indels 5; Gaps 3;

QY      306  GTCGTGCGGACGAGTGTGTCGCGCTGCGTACCAAGGGAAACAGTCGCGCTCGGTGCGGA 365
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DB      62  GTCGTGCGCGGTGTGTGTCGCGGTGCGTACCAAGGGAAACAGTCGCGCTCGGTGCGGA 121
        |||||||

QY      366  CTGGCTGAAACAAGGGGGAACAAGCGCTGTGAGCACTGTGTGGCGGACGCTGTGGGCTGCA 425
        |||||||
DB      122  CTGGCTGAAACAAGGGGGAACAAGCGCATGTGTGTGGCGGACGCTGTGGGCTGCA 181
        |||||||

QY      426  GAGCGTGCAGGCTTGTGTGCTGTACGAGCGCGGTGTGAAGAAGAAGTGGCGGCTGAA 485
        |||||||
DB      182  GAGCGTGCAGGCTTGTGTGCTGTACGAGCGCGGTGTGAAGAAGAAGTGGCGGCTGAA 241
        |||||||

QY      486  CTCGGGCTTCATGTGCGCTCTACGCCCTTCGCGCGGTGTGATCTGCTGGGTCACTGGGC 545
        |||||||
DB      242  CTCGGGCTTCATGTGCGCTCTACGCCCTTCGCGCGGTGTGATCTGCTGGGTCACTGGGC 301
        |||||||

QY      546  GTACCAACATGTGTTGGGGAGAAGCTCTCTCCGATCTGGGGGAAGCGCGGCTGCT 605
        |||||||
DB      302  GTACCAACATGTGTTGGGGAGAAGCTCTCTCCGATCTGGGGGAAGCGCGGCTGCT 361
        |||||||

QY      606  GGACCAAGGCTCTCTGTCGCGCGCGCGCGGTGCGGCGAAGGTCCACTACCGCGCGA 665
        |||||||
DB      362  CAACCAAGACTCTCTGTCGCGCGCGCGCGGTGCGGCGAAGGTCCACTACCGCGCGA 421
        |||||||

QY      666  CGGCAAGCTGTGAGACGGCGCGGTGAGCGCTGTACCCGATGCGACGCGGTGTACTT 725
        |||||||
DB      422  CGGCAAGCTGTGAGACGGCGCGGTGAGCGCTGTACCCGATGCGACGCGGTGTACTT 481
        |||||||

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QY      726  CCAAGTGGCTGTTGCGCGGCATCACCTCATCTGTGCGCGGCTCCCTCTCGGCGCGAT 785
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        |||||||

QY      786  GAGCTTCTCTGCTGATGATCTTGTGTCGCTGTGCTACCTTCTCTACACCGTC-G 844
        |||||||
DB      542  GAGCTTCTCTGCTGATGATCTTGTGTCGCTGTGCTACCTTCTCTACACCGTCG 601
        |||||||

QY      845  GCGCTTCTCTCTGCTGCGG--CGCGGCTTCTCTTCCACTGGGG--CGTATGACTAC 900
        |||||||
DB      602  GCGCTTCTCTCTGCTGCGGCGCGGCTTCTCTTCCAGTGGGCGGTGATGACTAC 661
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QY      901  TCGCGCGGCTACG 913
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DB      662  TCGCGGCGCTACG 674
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Search completed: July 24, 2006, 00:33:03
Job time : 16358 secs

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Db	83	GTCGGGGAAGATGTGCTGTCGCGGTGGCGGTACCAAGGGGAACGTCGCGCGCGGTGGCGGA	142
OY	366	CTGGCTGAAACCAAGGGGAACAACGCGTGGAGCTGGTGGCGCGGACCGCTGGTGGGGCTGCA	425
Db	143	CTGGCTGAAACCAAGGGGAACAACGCGTGGAGCTGGTGGCGCGGCTGCACTGGTGGGGCTCAT	202
OY	426	GAGCGTGCCGGGCGTTGTGTGTCTGTACGGCGGCGCTGTGAAGAAGAACTGGCGGTGAA	485
Db	203	GAGCGTGCCGGGCGATGTGTGTCTGTACGGCGGCGCTGTGAAGAAGAACTGGCGGTGCAA	262
OY	486	CTGGCGCGTATATGAGCGCTCTACGAGCTTCGCGCGCGCTGTGAGATCTGCTGGGTCACTGAGCG	545
Db	263	CTCGCGCTTCAATGGCGCTTACGCGCTTGCGCGCGCTGTGAGATCTGCTGGGTGCTCTGAGCG	322
OY	546	GTACACATGTGCTTTGGGGGAAGTCTCTCCGATCTGGGGGAAGGCGCGGCGGGCGCT	605

Db 323 CTACAACATGTCCTTCGCGAGAGAGTGTCTCCGTTCTGCGGCAAGCCGCGCGCGCT 382
QY 606 GGACCAAGGCGCTTCCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 665
Db 383 CGACCAAGGCGCTTCCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 442
QY 666 CGGCAAGCGTGAAGAGCG 725
Db 443 CGGCAAGCGTGAAGAGCG 502
QY 726 CCAAGTGCCTGTCG 785
Db 503 CCAAGTGCCTGTCG 562
QY 786 GAGCTTCCTGCG 845
Db 563 GAGCTTCCTGCG 622
QY 846 CGGCTTCCTGCG 905
Db 623 CGGCTTCCTGCG 682
QY 906 CGGCTTCCTGCG 965
Db 683 CGGCTTCCTGCG 742
QY 966 TACTAACAGC 975
Db 743 GCCAAGAGCC 752

RESULT 2
US-10-033-109-9
; Sequence 9, Application US/10033109
; Patent No. 6833492
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; PRIORITY FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1883
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-033-109-9

Query Match 10.6%; Score 389.2; DB 3; Length 1883;
Best Local Similarity 74.0%; Pred. No. 5.5e-70;
Matches 493; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 297 GAAGATGTGCTGCTCGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 356
Db 74 GAAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 133
QY 357 GGTGGCGAGCTGCTGAACAAGGAGCAACGCGTGGCAGCTGTGTGGCGGCGAGCGTGT 416
Db 134 GGTGGCGAGCTGCTGAACAAGGAGCAACGCGTGGCAGCTGTGTGGCGGCGAGCGTGT 193
QY 417 GGGGCTGCAAGAGCGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 476
Db 194 CGGGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
QY 477 GGGGCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536

Db 254 GGCGGTCACTCGGCTTCATGCGCTGTGACGCGTACCGGTCAACGCTCATCTGTGGGT 313
QY 537 CACCTGGCGCTTCAACATGTGTTCGCGGAGAGAGCTCTCTCCGATCTGCGGAGAGCGG 596
Db 314 GCTGTGCGCTTCGCGATGTGTTCGCGGAGAGAGCTCTCTCCGATCTGCGGAGAGCGG 373
QY 597 GCGGCGCTGAGACGAGGCGCTCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 656
Db 374 GCGGCGCTGAGAGAGGCGCTCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 433
QY 657 CCGGCGCGAGCGAGCGGTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 716
Db 434 CCGGAGAGAGCGGCG 493
QY 717 GGTGACTTCAGTGTGTGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 776
Db 494 GGTGTGTTCAGTGTGTGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 553
QY 777 CGGCGCGATGAGCTTCG 836
Db 554 CGGAGAGATGAACATCAAGGCGGTGATGCGCTTCACTCGCTGCGCTCTCTCTCTCT 613
QY 837 CACGCTGCGCGCTTCCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 896
Db 614 CACGCTGCGCGCTTCCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 673
QY 897 CTACTGCT 956
Db 674 CTACTGCT 733
QY 957 CTGGGT 962
Db 734 CTGGGT 739

RESULT 3
US-10-033-109-11
; Sequence 11, Application US/10033109
; Patent No. 6833492
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; PRIORITY FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1961
; TYPE: DNA
; ORGANISM: Glycine max
US-10-033-109-11

Query Match 7.9%; Score 289.6; DB 3; Length 1961;
Best Local Similarity 67.0%; Pred. No. 1.6e-49;
Matches 409; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 353 CGTGCTGCGAGCTGCTGAACAAGGAGCAACGCGTGGCAGCTGTGTGGCGGAGCGC 412
Db 248 CGGCGGCAACCCCAATGGCTGAACAAGGTGACCAAGCATGTGAGCTTAACAGCACGCC 307
QY 413 TGTGTGGGTGAGAGCGGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 472
Db 308 TGTGTGTGTTAAGCATGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 367
QY 473 AGTGGCGGTGAACCTCGCGCTTCATGCGGCTTACGCGCTTGGCGCGCGGTGTGTGTGT 532

Db	368	AATGGGCAAGAACTCAGCTTTCATGGCTCTCTCAAGCCTTTGGCGGCTTCAATATGTT	427
Oy	533	GGGTCACCTGGGGGTCAACATGTCGTTGGGGGAGAGCTCTCCGATCTGGGGGAAAG	592
Db	428	GGGGCTTGTGTGTATCCGATGGCTTTGGAGAAAGACTTTTCCCTTCTGGGGAAAG	487
Oy	593	CGCGGCGGCGGCTGAGCAAGGGGCTTCGTGGCGGCGCGCGCTGCGGCGAGCGGTCC	652
Db	488	GTGCTCAGCAGCTAAGGCGAAGATTCTCAGCAAAAAGACATGATCATTAAGCAATCC	547
Oy	653	ACTACCGCGCCCAACGGCAGCGTGGAGACGGCGGCGGTGAGCGCGGTGATCCCATGGCGA	712
Db	548	ACACCTTTGATATATGGCACGTGGATCACTTCGAGGAACCTTTTACCTTAATGAGCTT	607
Oy	713	CGGGTGTACTTCCAGTCGCTGTTGGCGGCATCACTCATCTCTGCTCCGCGCTCC	772
Db	608	CGCTGTGTATTTCCAAATTCACTTTGTGCTGATTAATCTTAATTTGTGTGGCTGGCTGG	667
Oy	773	TCTCGGCGGCAGTAGAGCTTCCTGCTGGATGATCTTGTCCGCTCTGGGCTACCTTCT	832
Db	668	TCTTGGCCCAATGAACATCAAGGCTGGATGGCTTTGTGTGCTTTGTGTGATCTTTT	727
Oy	833	CCTACACGTCGGCGGCTTCTCCCTCTGGGGGCGGCGGCTTCTCTTTCACCTGGGAGCTCA	892
Db	728	CTTACACAGTCGGGGCTTTAGCTTTTGGGGTGGTGCTTTCTTACCAATGGGGCGTGA	787
Oy	893	TCGACTACTGCGGCGGCTACGTCATCAACGTCCTCGCGGCAGTCGCGGCTTCAACCGCG	952
Db	788	TTGATTTTCTGGCGGCTATGTCATCACTTCTTCTGGAACTCGCTGGCTTCACTGCTG	847
Oy	953	CTTACTAGGCT 962	
Db	848	CTTACTAGGCT 857	

RESULT 4
US-10-033-109-7
; Sequence 7, Application US/10033109

```

1 GENERAL INFORMATION:
2 APPLICANT: Allen, Stephen M.
3 APPLICANT: Rafalski, J. Antoni
4 APPLICANT: Sakai, Hajime
5 TITLE OF INVENTION: Nitrogen Transport Metabolism
6 FILE REFERENCE: BB-1210
7 CURRENT APPLICATION NUMBER: US/10/033,109
8 CURRENT FILING DATE: 2001-12-28
9 PRIOR APPLICATION NUMBER: 09/384,625
10 PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
11 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
12 PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
13 NUMBER OF SEQ ID NOS: 14
14 SOFTWARE: Microsoft Office 97
15 SEQ ID NO 7
16 LENGTH: 376
17 TYPE: DNA
18 ORGANISM: Zea mays
19 FEATURE:
20 NAME/KEY: unsure
21 LOCATION: (40)
22 NAME/KEY: unsure
23 LOCATION: (272)
24 NAME/KEY: unsure
25 LOCATION: (276)
26 NAME/KEY: unsure
27 LOCATION: (294)
28 NAME/KEY: unsure
29 LOCATION: (339)
30 NAME/KEY: unsure
31 LOCATION: (341)
32 NAME/KEY: unsure
33 LOCATION: (359)
34 NAME/KEY: unsure

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LOCATION: (361)
US-10-033-109-7

Query Match	5.2%	Score 190.2;	DB 3	Length 376;
Best Local Similarity	74.5%	Pred. No. 1.9e-29;		
Matches 277;	Conservative	0;	Mismatches 85;	Indels 10; Gaps 3;

OY	239	GCATGCTAGAGATATCCAAAAGAAAGCATATCCAAAGCTTAGTGTGTGATATCAGACGCA	298
Db	1	GCTTAAGAGAGAGAGAGAGAGAGATATATCTTAGAACCGAGCGCAACTAGCTAATCTAAC	60
OY	299	AGATGTCGTCTGTCGCGGACGAGTGATGCGCGTGGCGTACCAAGGGAGAACATCGCGCTCGG	358
Db	61	TGTCGTCTGTCGTCTCGGAGAGAGATGCGCGTGGCGTACCAAG-----ACGTCGCGCTGCT	114
OY	359	TGCGCGACTGCGCTGAACAAAGGGGAGCAACGCGTGGCAGCTGTGTGGCGGCGACGCTGGTGG	418
Db	115	CTCCCAAGTGGCTGTGAACAAAGGGCGCAACAACGCGTGGCAGCTGACCGCGCGCAACGCTGGTGG	174
OY	419	GGCTGAGAGCGCGGCCGCTTGGTGGTGGCTGTACCGCGCGCGTGGTGAAGAAGATGGG	478
Db	175	GGCTGAGAGCTTCCGGGCTCTGTGTGTCTGTATACGCGCGCGCTGTGTGAAGAAGATGGG	234
OY	479	CGGTGAACCTCGCGCTCATGCGGCTCTACAGCGCTTCCGCGCC--GTGTGATCTGCTGGGT	536
Db	235	CGGTGAACCTCGCGCTCATGCGGCTGTACGGCTTCCGCGCGGAGTGTGGATCTGCTGGG	294
OY	537	CACCTGGGCGGTACAACATGTGTTGGGGAGAA--GCTCTTCCGATCTGGGGAGAGCG	594
Db	295	GACCTGGGCGCTACAACATGTCTTTGGCGAAACAGGCTGTGTGNTGTTGGGGCAAGG	354
OY	595	CGCGCGGCGCTG	606
Db	355	CGGAGNACGATG	366

RESULT 5
US-09-197-649-7/C

```

? Patent No.: 5194550
? GENERAL INFORMATION:
? APPLICANT: Gold, Larry
? APPLICANT: Tuerk, Craig
? APPLICANT: Pribnow, David
? APPLICANT: Smith, Jonathan D.
? TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
? FILE REFERENCE: NEX02/C1-CON
? CURRENT APPLICATION NUMBER: US/09/197,649
? CURRENT FILING DATE: 1998-11-23
? EARLIER APPLICATION NUMBER: 07/829,461
? EARLIER FILING DATE: 1992-01-31
? EARLIER APPLICATION NUMBER: 07/739,055
? EARLIER FILING DATE: 1991-08-01
? EARLIER APPLICATION NUMBER: 07/561,968
? EARLIER FILING DATE: 1990-08-02
? NUMBER OF SEQ ID NOS: 26
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 7
? LENGTH: 390
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Sequence
? OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
? OTHER INFORMATION: fragments having NcoI restriction sites.
? US-09-197-649-7

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[illegible]

[illegible]

```

RESULT 6
US-09-252-991A-7174
; Sequence 7174, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7174
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7174

```

	Query Match	3.1%	Score 112.8	DB 3	Length 1366
	Similarity	51.2%	Pred. No.2.9e-13		
	Match	338	Conservative	0	Mismatches 292; Indels 30; Gaps 2
Qy	298	AAGATGTCGTCTCGGCGACGGTGTGTCCGCTGAGCGTACCAAGGGAACAAGTCGGCGTGC	357		
Db	52	AAGATCGCAGGGCTFAGGAGCCCTATTGTTCCTCGCTTTCGCGGCGTGCCTTCGCGCGCC	111		
Qy	358	GTGGCGGACTGGCTTAAACAAGGGGGAACAAGCGTGGCAGCTGTGTGGCGCGACCGCTGTGG	417		
Db	112	GAGGAGCCCGTCTTAACACGCGGCACACCGCTGGATCTATCTCACTGCGCTCGTC	171		
Qy	418	GGGCTGCAGAGCGTGC CGGGCTTGTGTGTCTGTACCGGCGGCGTGTGAAGAAAGTGG	477		
Db	172	CTGCTCATGACCATCTCCGCGCTTGCGCGCTTCTFACGGGCGCATGTGTGAGCAAGAAAC	231		
Qy	478	GCGGTGAACCTGGCGCTTATGAGCGGCTTACAGGCTTTCGCGCGCGGTGTGATCTGCTGGGTC	537		
Db	232	GTGCTGTGCATCATATGACGATGCTTTCGCTATCACCGGCTGTATCAACCAATTCTTGGGTG	291		
Qy	538	ACCTGGGCGGTACACATATGCTGTTGGGGGAGAAGCTTCTCCGATCTGGGGGAAGGCGCG	597		
Db	292	GCTATATGCTACAGGCTGGCGCTTTCATACCA-----CCGGG	327		

QY	598	CGGGCGCTGAGACAAAGGGCCCTCTCGTGGAGCCGCGCGCTGCGGGGAGCGTCACTAC	657
Db	328	ATGAGAAAGGGCTCTCTCAACTTCAATTCTTTCGTGGCGGAGCTGGACAAGGCTTCTC	387
QY	658	CGCGCGCAGCGCAGCGCTGAGAGACGGCGGCGGTGAGCCCGTTACCCGATGGCGACGGTG	717
Db	388	AGCGGTCTCACCGCCCGACGGCTGTACTTCGCGCACCGCGCGCTGTCCGGAAGCGGTTC	447
QY	718	GTCGACTTCCAGTGGCGGTGTTCGCGCCGCACTCACTCTCGTGGCGGCTCCCTCTC	777
Db	448	ATCACTTCCAGATATACCTTTGGGATATATCACTCGGCGGTGATGCTGGGGCTTTCGCC	507
QY	778	GGCGCGATAGCTTCTCGCTCGATGATCTTTCGTCCGCTCTGGCTCACTTCTCTAC	837
Db	508	GACCGCATGAAGTTCTCGGCGATGTGATCTTCAATGGGAGCTGTGTTACCGTGTAC	567
QY	838	ACCGTCGGCGCTTCTCTCTCTG-----GGCGGCGCTTCTCTTCACTGGGCGCTC	891
Db	568	GCGCCGATGGCGGACATGGTCTGGAGCGGTGACGGCGCCCTGATGTGGACTGGGCGTG	627
QY	892	ATGACTACTGGCGGGGAGTCACTCATCCAGCTTTCGCGGCAATCGCGGCTTCAACGCC	951
Db	628	CTGACACTTGGCGCGCGCACCGTGTGATCAACGCGGGATATCGCGGCTCTGTGGCC	687

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RESULT 7
US-09-252-991A-7330/C
; Sequence 7330, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7330
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7330

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	Query Match	3.0%: Score 111.8; DB 3; Length 1515;
	Best Local Similarity 51.7%: Pred. No. 5e-13;	
	Match 328; Conservative 0; Mismatch 277; Indels 30; Gaps 2;	
QY	323 TGCCGCTGGCTACCAAGGGGAAACAAGTCGGCGTGGTGGCGACTGTGCTGAACAAGGGG	382
DB	1571 TGTCCCTGGCTTTGCCGGGCGTCCCTCGGCCGCCGAGGAGCCGCTCTGAACAGCGCG	1512
QY	383 ACAACGCTGGCACTGTGTGGCGGCAAGCTGTGTGGGGCTTGCAGAGGTGCGGGGCTTTGG	442
DB	1511 ACACCGCGCTTGATCTGATCTCCACTCGCTCGCTCTGCTATACCATCCCGCGGCTGG	1452
QY	443 TGTGTGCTGACGGGGCGCTGTGAAGAAAGTGGGCGGTGAACCTCGGCTTCATGCGCG	502
DB	1451 CGCTGTTCTACGGGGGCGCATGTGTGGACGAAAGAACTGTCTGTGATATATGACAGTGCT	1392
QY	503 TCTAAGCCTTGGCGCGCTGTGATCTGTGGGTCAACTGTGGCGCTACAACTGTGTTGG	562
DB	1391 TCGCATACACGGGCTGATCAACATTTCTGTGGGTGTCTATGTGCTACAGCGCTGGCGTTGG	1332
QY	563 GGGAGAACTCTCTCCCATCTGTGGGGAAAGGCGCGCGGCGCTGTGACAGGCGCTCTCTGG	622
DB	1331 ATACCA-----CCGGGATGAGAAAGGCGGTCTCTCAACTTCA	1296
QY	623 TCGGCGGCGCGCGCTGCGCGGACGATCCACTACCGCGCGACGCGAGCGCTGTGAGACGG	682

QY 3186 AACGTGTGTGACCTCTCCCTCATCTGTGCGCATCAACTCTCTGTCGCCGCTCCGCAAG 3245
DB 1189225 GTGCGCGCGACACCCGCTACCCCTTATCCGGGGTGGCCACGACATGTTGCGCGCC 1189284
QY 3246 CCCGACGACAAAGTGTGAGGTGCGCGACGACGCGCTCCACCGCGAGAGAGCGCTACGCGCTC 3305
DB 1189285 GGGCGCGCGCGCGCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCTGTACCTCCGTGACC 1189344
QY 3306 TGGGCGACGCGCGAGATGTACGACGTCACCAAGACCGCTCCGACGCGCGCGCTTGGCCCCC 3365
DB 1189345 GAACAGACGCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCC 1189404
QY 3366 GTGTGTGTATGATGATCATCATTAATTAATGATGTGCTGTACCC 3407
DB 1189405 GGTGCGCGCGCTGTCCACCGAATTGGCGCGCGCTTGGCGCGACCC 1189446

RESULT 13

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: FRASER, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 2.4%; Score 90; DB 3; Length 4411529;
Best Local Similarity 51.5%; Pred. No. 8.2e-07;
Matches 207; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 3006 GTCTTCACACCCACGCGGTGCGCGCTCTCTGCGCGCTCTCTCAACCGGCTCTTTCGCC 3065
DB 1189019 GCGGCGCGACCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1189078
QY 3066 GAGCCCAACCTGTGCAACTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3125
DB 1189079 GTTACCACTAGTGGCGCGCTTGAAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1189138
QY 3126 GGGCG 3185
DB 1189139 GCGGCG 1189198
QY 3186 AACGTGTGTGACCTCTCCCTCATCTGTGCGCATCAACTCTCTGTCGCCGCTCCGCAAG 3245
DB 1189199 GTGCGCGCGACACCCGCTACCCCTTATCCGGGGTGGCCACGACATGTTGCGCGCC 1189258
QY 3246 CCCGACGACAAAGTGTGAGGTGCGCGACGACGCGCTCCACCGCGAGAGCGCTTACGCGCTC 3305
DB 1189259 GGGCG 1189318
QY 3306 TGGGCGACGCGCGAGATGTACGACGTCACCAAGACCGCTCCGACGCGCGCGCTTGGCCCCC 3365
DB 1189319 GAACAGACGCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCC 1189378
QY 3366 GTGTGTGTATGATGATCATCATTAATTAATGATGTGCTGTACCC 3407
DB 1189379 GGTGCGCGCGCTGTCCACCGAATTGGCGCGCGCTTGGCGCGACCC 1189420

RESULT 14

US-09-023-173-4
; Sequence 4, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; NUMBER OF SEQUENCES: 23
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

ZIP: 94306
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,168
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petichory, Joanne R
; REGISTRATION NUMBER: P42995
; REFERENCE/DOCKET NUMBER: 0665-0007.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: codon-optimized Ramy3D signal-prosultilin BPN'
US-09-023-173-4

Query Match 2.4%; Score 89.8; DB 3; Length 1140;
Best Local Similarity 52.2%; Pred. No. 1.4e-08;
Matches 199; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 2993 CGACACCTTGCGCGGTTCACACCCACGCGCGGTGCGCGCTCTCTGCGCGCGCTCTCTCAC 3052
DB 465 CGAGACCAACCGGTTCAGAGACCAACAGACATGACACCAACGTCGCGCGCGCGCGCGCGCG 524
QY 3053 CGGCTCTTTCG 3112
DB 525 CGGCTCTTTCAGACAGCATGCGGTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 584
QY 3113 CGGCTCTTTCAGACAGCATGCGGTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3172
DB 585 CAAGTACTTGGCG 644
QY 3173 CGTGTGCGCTGGAAGTGTGTGTCACCTCTCTCATCTGTGCGCATCAACTCTCTCTCTCTCT 3232
DB 645 GGGCATTCGCAACATGAGCGTATCACTATGAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCG 704
QY 3233 CCGGCTCTGCG 3292
DB 705 CGGCTCTTTCAGAGCGCGGTGTGACAGAGCGCGGTGTGCGCGCGCGCGCGCGCGCGCGCGCG 764
QY 3293 GGGCTTTCG 3352

Db 765 CGGCAACGAGGCGACCGGCGAGCAGACCGTCGCGCTACCGGCAAGTACCGGAG 824
QY 3353 CGCCGTTGCCCCGTCGTGTGT 3373
Db 825 CGTCATCGCGCTGCGGCGCGCT 845

Job time : 1213 secs

RESULT 15

US-09-974-300-5249/C
; Sequence 5249; Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Method For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/580,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5249
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(863)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5249

Query Match 2.4%; Score 89; DB 5; Length 863;
Best Local Similarity 51.3%; Pred. No. 1.8e-08;
Matches 231; Conservative 0; Mismatches 216; Indels 3; Gaps 1;

QY 2923 TCGCCGCGAGCATCCCGTGATACCATGATGTCCTCCACAGCGCTCCAGATCTGCG 2982
Db 575 TCAGCGTCCGAACTCCGCATCCGCATCGGCGTCGCGATCCGCATCGGCATCGCGCG 516
QY 2983 AGCGCGTCGACGACACCTTCGCGGCTTTCACACCGACGCGCGCGGCTTCCTCGCG 3042
Db 515 TCAGCATCAGCGTCGCGATCGGCTGCGATCGGCATCGGCATCGGCATCGGCATCGCA 456
QY 3043 GCCTCTCAACGCGCTCTTCGCGGAGCCACCTCTGCAACCTTCTCCCGTCCGCG 3102
Db 455 TCGCATCGGCGTCCGCATCCGCATCGCATCGCATCGGCATCGGCATCGCATCGCG 396
QY 3103 ACTCCGCGGCGCTTCTACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3162
Db 395 TCGGCATCGGCGTCCGCATCCGCATCGCATCGCATCGCGCATCGCGCATCGCGCG 336
QY 3163 GCGGCGCTTTCGTCGTCGCGCGTGGAGATGTCGTCACCTCCATCTGCGCTGCGCATCA 3222
Db 335 TCGCATCCGCATCCGCGTCCGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 279
QY 3223 ACTCTCTGTCGCGCTTCGCGATCGCGATCGCGAGACAACTCGAGTGGCGAGCGCGTCC 3282
Db 278 GCGTCGCGCTCGGCATCGGCATCGCGTCCGCGATCGCGATCGCGATCGCGCGTCC 219
QY 3283 AGCGCGAGAGGCTTACGCGCTTGGGCGACGCGGAGATGTACAGCTACCAAGCAGC 3342
Db 218 GGTTCAGCATCAGCATCAGCATCAGCGTCCGCGTTCGCGCATCCGCATCCGCATCCAGCTCC 159
QY 3343 GCTCCGACGCGCGCTTGGCGCGCGCGCTGCG 3372
Db 158 GCATCGCGCTCAGCGCTCGGCATCGGCATCG 129

Search completed: July 23, 2006, 15:40:17

Db	122	GAA	CAAGGGCGA	CAAGCGTGG	CACTGGTGGCGG	GACGCGTGGTGGGGCTGG	CAGACCGT	181
Qy	432	GCGGGGCTTGGTGGTGGTCTG	TACGGCGGGCGTGGTGA	AGAAAGTGGGGCGTGA	CACTCGGC	493		
Db	182	GCGGGGCTTGGTGGTGGTCTG	TACGGCGGGCGTGGTGA	AGAAAGTGGGGCGTGA	CACTCGGC	241		
Qy	492	GTTTCATGGCGCTCTTA	CGCCTTGGCGCGCGTGGAT	CTGTCTGGGTCA	CTTGGGGGTCA	551		
Db	242	GTTTCATGGCGCTCTTA	CGCCTTGGCGCGCGTGGAT	CTGTCTGGGTCA	CTTGGGGGTCA	301		
Qy	552	CATGTCTGTTGGGGAGA	AGCTCTCCCGATCTGGGGAGA	AGCGCGCGCGCTGGACA	611			
Db	302	CATGTCTGTTGGGGAGA	AGCTCTCCCGATCTGGGGAGA	AGCGCGCGCGCTGGACA	361			
Qy	612	GGGCTTCCTGTGGCGCGCGCGCGCTG	CGCGGACGCTCCACTACCGCGCCGACGGCAG	671				
Db	362	GGGCTTCCTGTGGCGCGCGCGCGCTG	CGCGGACGCTCCCGACGCTCCACTACCGCGCCGACGGCAG	421				
Qy	672	CGTGGAGA	CGGCGGCGTGGAGCGCTGA	ACCGATGGCGACGGTGGTACTTCA	AGTG	731		
Db	422	CGTGGAGA	CGGCGGCGTGGAGCGCTGA	ACCGATGGCGACGGTGGTACTTCA	AGTG	481		
Qy	732	CGTGTTCGCGGCATCA	CCCTCACTCTGATGCGCGCTCTCCCTCGGCGCATGA	CTT	791			
Db	482	CGTGTTCGCGGCATCA	CCCTCACTCTGATGCGCGCTCTCCCTCGGCGCATGA	CTT	541			
Qy	792	CTTCGCGCTGGATATCT	TGTCCTCCGCTCGGCTCA	CACTTCCCTCA	CAACCGTCGGCGCTT	851		
Db	542	CTTCGCGCTGGATATCT	TGTCCTCCGCTCGGCTCA	CACTTCCCTCA	CAACCGTCGGCGCTT	601		
Qy	852	CTCCCTTCGGGGCGGCGGCTT	CTCTTCCACTGGGGCGTCA	CTGACTTCTGCGCGGCTA	911			
Db	602	CTCCCTTCGGGGCGGCGGCTT	CTCTTCCACTGGGGCGTCA	CTGACTTCTGCGCGGCTA	661			
Qy	912	CGTCAATCA	CGCTTCCGCGGACATGCGCGGCTT	CAACCGCGCTTACTGGATCCGTA	970			
Db	662	CGTCAATCA	CGCTTCCGCGGACATGCGCGGCTT	CAACCGCGCTTACTGGATCCGTA	720			

RESULT 2
US-10-033-109-13
Sequence 13, Application US/10033109
Publication No. US20020142390A1
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Rafaleki, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/10/033,109
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 1656
TYPE: DNA
ORGANISM: Trillium aestivum
US-10-033-109-13

Query Match	14.4%;	Score 529.2;	DB 6;	Length 1656;
Best Local Similarity	86.9%;	Pred. No. 9.3e-94;		
Matches 582;	Conservative 0;	Mismatches 88;	Indels 0;	Gaps 0;

Oy		366	GTCGCTGGACAAAGGGGCAACAACCGGTGGCAGCTGGTGGCGGAGACGCTTGTTGGGGCTTGC	425
Oy		306	GTCGTCGGCCACGATGTGTCGCCCTGGCGATTACCAGGGGAACACTGTGGCGTGGTGGCGGGA	365
Dd		83	GTCGGGCAAGATGTCGGTGGCCGGGTGGCGTTAACAGGGGAAACAAGTGGCGCGCGTGGCCGA	142

Db	143	CTGGCTGAACAAGGCGCAGACACGCTGGCAGCTGACGGCGTCCACGCTGCTGGGCTCAT	202
QY	426	GAGCGTGC CGGAGCTTGTGTGTCTGTACCGCGGCGGTGTGAAGAAAGAGTGGGCGGTGA	485
Db	203	GAGCGTGC CGGAGCATGTGTGTCTGTACCGCGGCGTGTGAAGAAAGAGTGGGCGGTCAA	262
QY	486	CTCGGCGCTTAAATGGGGCTCTAAGCCTTGGCGCGCGGTGTGATCTGTGGGTCAACCTGGAG	545
Db	263	CTCGGCGCTTAAATGGGGCTCTAAGCCTTGGCGCGCGGTGTGATCTGTGGGTGTCTGGGCG	322
QY	546	GTACAACATGTGTCTTCGGGAGAAAGCTCTCTCCGATCTTGGGGAAAGCGCGGCGCGCT	605
Db	323	CTACAACATGTGTCTTCGGGAGAAAGCTCTCTCCGATCTTGGGGCAAAAGCGCGGCGCGCT	382
QY	606	GGAACCAAGGAGCTCTCTGTGTGTGGCGCGCGCGGTGTGCGCGGAGAGGTTCATTACCGCGCGCA	665
Db	383	CGACCAAGGAGCTCTCTGTGTGTGGCGCGCGCGGTGTGCGCGGAGAGGTTCATTACCGCGCGCA	442
QY	666	CGGACGAGTGGAGACGGGCGGCGGTGGAGCGCGGTGTACCCGATGGCGACGGTGGTACTT	725
Db	443	CGGACGAGTGGAGACGGGCGGCGGTGGAGCGCGGTGTACCCGATGGCGACGGTGGTACTT	502
QY	726	CCAGTGGGTGTTCGCGCGCATCACCCTCATCTCTGTGTGCGCGGCTCTCTCGGCGCGCAT	785
Db	503	CCAGTGGGTGTTCGCGCGCATCACCCTCATCTGTGTGCGCGGCTCTCTCGGCGCGCAT	562
QY	786	GAGCTTCTCGCGGTGATCTTGTGTGCGCGGTGGGCTACCTTCTCTTACACCGTGGG	845
Db	563	GAGCTTCTCGCGGTGATCTTGTGTGCGCGGTGGGCTACCTTCTCTTACACCGTGGG	622
QY	846	CGCCTTCTCCCTCTGGGGCGGCGGCTTCTCTTTCACATGGGGCGTATGACTTACGCGG	905
Db	623	CGCCTTCTCCGTTGTGGGGCGGCGGCTTCTCTTTCACATGGGGCGTATGACTTACGCGG	682
QY	906	CGGCTACGTATCACGTTCTCGCGCGCATGCGCGGCTTACACCGCGGCTTACTGGGTCCG	965
Db	683	CGGCTACGTATCACATCTCCGCGCGGCGGTGCGCGGCTTACACCGCGGCTTACTGGGTCCG	742

```

RESULT 3
US-11-012-668-13
; Sequence 13, Application US/11012668
; Publication No. US20060010512A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/11/012,668
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
;
; LENGTH: 1656
; TYPE: DNA
; ORGANISM: Trifolium aestivum
US-11-012-668-13

```

Query Match	14.4%	Score 529.2;	DB 16;	Length 1656;
Best Local Similarity	86.9%	Pred. No. 9.3e-94;		
Matches 582;	Conservative	0;	Mismatches 88;	Indels 0;
				Gaps 0;

Qy	306	GTCTGCGCCAGCGTGTGTGCTGCTGGCGTACAGGGGAAACAGTGTGGCGTGTGGTGGCGA	365
Dh	83	GTCTGGCAACATGTCTGGTGGCGTGTGGCGTACAGGGGAAACAGTGTGGCGTGTGGTGGCGA	142

Db 113 AGAGAGAGTATACGTAGGACCGCGCGGACCACTTAACAATGTCGTGCTCCG 172

QY 315 GACGCTGTGTCCTGCGCTGACCAAGGGAAACAGTTCGGCTCGGTGCGGACTGGCTGAA 374

Db 173 GACGACGATGCGCTGCGCTACAG-----ACGTGGCGGTCTCTCCCAAGTGGCTGAA 226

QY 375 CAAGGGGGGACAAACGGGTGGCAGCTGGTGGCGGCGACGCTGTGGGGCTGCAGAGCGGCC 434

Db 227 CAAGGGCGACAAACGGGTGGCAGCTGACGCGCGGCGACGCTGTGGGGCTGCAGAGCTTCCC 286

QY 435 GGGCTTGTGTGTGCTGTACGCGCGCGTGTGAAAGAAATGTGGCGGTGAATCTCGGCTT 494

Db 287 GGGTCTGTGGTGGTCTGTACGCGCGCGTGTGAAAGAAATGTGGCGGTGAATCTCGGCTT 346

QY 495 CATGGCGCTTACGCTTTCGCGCGCTGTGTGATCTGCTGGGTACCTTGGGCGTAAACAAT 554

Db 347 CATGCGCTGTACGCGCTTTCGCGCGGTGTGATCTGCTGGGTACCTTGGGCGCTTAACAAT 406

QY 555 GTGCTTGGGGGGAAGCTCTCCCAATCTGGGGGGAAGCGCGGCGCGGCTTGACCAAGG 614

Db 407 GTCTTTCGCGCAACAGCTGTCTGCTGTGGGGCAAGCGCGGCGCGGCTTGACCAAGG 466

QY 615 CCTCTCTGTGCGCGCGCGCTGCGCGCAACGATCACTACCGCGCGCAAGCGT 674

Db 467 CTGCGTGTGGTGGGGCAGGGCGGGCTCCCGCGCAACGCGCAACATTTGGCGCGCGGCTT 526

QY 675 GGAGACGGCGCGCGGTGTGAGCCGCTGTACCCGATGTGGAGAGGTGTACTTCCAGTGGCT 734

Db 527 GGAGACCCCGCGCGCGAGCCGCTGTACCCGATGTGGAGAGGTGTACTTCCAGTGGCT 586

QY 735 GTTGGCGCGCATCACCCGTATCTGTGTGCGCGGCTCCCTCTCGGCGCGATGAGCTTCT 794

Db 587 GTTCCGCGCATCACCCGT 646

QY 795 CGCCTGTGATGTCTTCTGCTCGCGCTGTGCTCACTTCTCTTACACCGTGGCGCTTCTC 854

Db 647 CGCGGTGATGTCTTCTGCTCGCGCTGTGCTCACTTCTCTTACACCGTGGCGCTTCTC 706

QY 855 CCTTGGGGCGGGCTTCTCTTCCACTGTGGGGCGGTATGACTACTGTGGCGGCTTACGT 914

Db 707 CGTCTGGGGCGGGCTTCTCTTCCAGTGGGGCGGTATGACTACTGTGGCGGCTTACGT 766

QY 915 CATCACCTCTCGCGCGGATCGCGGCTTCAACCGCGGCTTACTGGGT 962

Db 767 CATCACCTCTCGCGCTTGTGCTTGGCGGTTCAACGAGCGCTTACTGGGT 814

RESULT 5

US-10-437-963-44521

; Sequence 44521, Application US/10437963

; Publication No. US20040123343A1

GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437, 963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

```

; LENGTH: 1497
;
; TYPE: DNA
;
; ORGANISM: Oryza sativa
;
; FEATURE:
;
; OTHER INFORMATION: clone ID: PAT_MRT4510_47574C.1
;

```

US-10-437-963-44521

Query Match 12.3%; Score 453; DB 8; Length 1497;

Best Local Similarity 81.8%; Pred. No. 9, 8e-79;

Matches 554; Conservative 0; Mismatches 105; Indels 18; Gaps 2;

```
QY 301 ATGTGTCGTGGCCACGCTGTGGCCGCTGGGCTGACGAGGGGACACGTCGGCGCGG 360
DB 1 ATGTGCGGGAGCGCTTCAACATGTGGGCGCTACACCC--TCGGGATGGCGGTG 57
QY 361 GCGGACTGCTGAACAAGGGGAGCAACGCGTGGCACTGGTGGCGCGACGCTGGTGGG 420
DB 58 CCGAGTGGCTGAACAAGGGGAGCAACGCGTGGCAATGATCTGGCGACGCTGGTGGG 117
QY 421 CTGCAGAGCTGCCCGGCTTGGTGTCTGTACGCGCGCGTGGTGAAGAAGTGGCG 480
DB 118 ATGCAGAGCTGCCCGGCTGGTGTGTCTGTACGCGCGCATGCTGAAGAAGTGGCG 177
QY 481 GTGAAGTGGCGCTTACATGGCGCTTACGCGCTTGGCGCGTGGATCTGGTGGTCAAC 540
DB 178 GTGAAGTGGCGCTTACATGGCGCTTACGCGCTTGGCGCGTGGATCTGGTGGTCAAC 237
QY 541 TGGGCGTACACATGCTGTTGGGAGAGCTCTCCGATCTGGGAGAGCGCGCGCG 600
DB 238 TGGGCGTACACATGCTGTTGGGAGAGCTCTCCGATCTGGGAGAGCGCGCGCG 297
QY 601 GCGCTGGACCAAGGCTCTCTCTGGCGCGCGCGCGCTGGCGCGCTCACT----- 655
DB 298 GCGCTGGGCGCAAGCTCTCTCTGGCGCGCGCGCTGGCGCGCTCACT----- 357
QY 656 -----ACCGCGCGAGCGCGAGCGCGAGAGCGCGCGCGTGGAGCGCGCTGTAAC 705
DB 358 AAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTAAC 417
QY 706 ATGGCGACGCTGCTGCTTCACTGCTGCTGCTTCCGCGCATGACCTCTCTCTGCGC 765
DB 418 ATGGCGACGCTGCTTCACTGCTGCTGCTTCCGCGCATGACCTCTCTCTGCGC 477
QY 766 GCGTCTCTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 825
DB 478 GCGTCTCTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537
QY 826 ACCTTCTCTTACACGCTGCGCGCGCTTCTCTCTGGGCGCGCGCTTCTCTTCACTG 885
DB 538 ACCTTCTCTTACACGCTGCGCGCGCTTCTCTCTGGGCGCGCGCTTCTCTTCACTG 597
QY 886 GCGCTCATGACTACTGCGCGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 945
DB 598 GCGCTCATGACTACTGCGCGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 946 ACCGCGCGCTTACTGGGT 962
DB 658 ACCGCGCGCTTACTGGGT 674
```

RESULT 6

US-10-425-115-73446

Sequence 73446, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 73446

LENGTH: 2130

TYPE: DNA

ORGANISM: Zea mays

FEATURE: OTHER INFORMATION: Clone ID: M74577_166983C.1

US-10-425-115-73446

Query Match 11.4%; Score 419; DB 9; Length 2130;

Best Local Similarity 79.8%; Pred. No. 6, 1e-72;

Matches 494; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

```
QY 344 AACGTCGCGCTCGGTGCGCGGATCTGGTGAACAAGGGGAGACACGCTGGAGCTGGTGG 403
DB 351 AGAGCTCTCTCGCGCTGCGCGGATCTGGTGAACAAGGGGAGACAAATGCGTGGAGTGA 410
QY 404 CGGCGAGCGTGGTGGGCTGAGAGCGCGCGGCTTGGTGTGCTGTGCTGCTGCTGCTGCT 463
DB 411 CCGGAGCGCTGGTGGGCTGAGAGCATGCGCGGCTTGGTGTGCTGTGCTGCTGCTGCTGCT 470
QY 464 TGAAGAGAGTGGGCGGTGAATCTGGCGCTTCACTGCGCTTCACTGCGCGCGCTGCTG 523
DB 471 TGAAGAGAGTGGGCGGTGAATCTGGCGCTTCACTGCGCTTCACTGCGCGCGCTGCTG 530
QY 524 GGAATCTGCTGGTCACTGGCGCTTCACTGCTTGGGAGAGAGTCTCTCCGATCT 583
DB 531 GGAATCTGCTGGTCACTGGCGCTTCACTGCTTGGGAGAGAGTCTCTCCGATCT 590
QY 584 GGGGAGAGCGCGCGCGCGCGCGCGCGCGCTCTCTGCTGCGCGCGCGCGCGCGCG 643
DB 591 GGGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 650
QY 644 CGACGCTCACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 703
DB 651 CGACGCTCACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 710
QY 704 CGATGGCGACGCTGGTGAATCTTCCAGTGGCGCTTGGCGCGCATCACTTCACTCTGCT 763
DB 711 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 770
QY 764 CGGCTCTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 823
DB 771 CGGCTCTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 830
QY 824 TCACCTTCTCTTACACGCTGCGCGCGCTTCTCTCTGGGCGCGCGCTTCTCTTCACT 883
DB 831 TCACCTTCTCTTACACGCTGCGCGCGCTTCTCTCTGGGCGCGCGCTTCTCTTCACT 890
QY 884 GGGGCGTCACTGACTACTGCGCGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 943
DB 891 GGGGCGTCACTGACTACTGCGCGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 950
QY 944 TCACCGCGCGCTTACTGGGT 962
DB 951 TCACCGCGCGCTTACTGGGT 969
```

RESULT 7

US-10-425-114-27103

Sequence 27103, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 27103

LENGTH: 1664

```

RESULT 8
US-10-033-109-9
; Sequence 9, Application US/10033109
; Publication No. US2002042390A1
;
GENERAL INFORMATION:
;
APPLICANT: Allen, Stephen M.
APPLICANT: Ratajski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/10/033,109
PRIORITY FILING DATE: 2001-12-28
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625S
PRIORITY FILING DATE: EARLIER FILING DATE: 1999-08-27
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248S
PRIORITY FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97

```

```

RESULT 9
US-11-012-668-9
; Sequence 9, Application US/11012668
; Publication No. US20060010512A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/11/012,668
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 16

```

SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1883
; TYPE: DNA
; ORGANISM: Oryza sativa
US-11-012-668-9

Query Match 10.6%; Score 389.2; DB 16; Length 1883;
Best Local Similarity 74.0%; Pred. No. 4,4e-66;
Matches 493; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

```
QY 297 GAAGATGTCGTCGTCGCGACGATGATGCGCTGCGGCTACAGAGGAACACGTCGCGCTC 356
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 74 GAAGAAGTAGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 133
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 357 GGTGCGGAGCTGCGCTGTAACAAAGAGGAGCAACCGCTGAGCTGCTGAGCGGCAACCTGCT 416
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 124 GGTGCGGAGCTGCGCTGTAACAAAGAGGAGCAACCGCTGAGCTGCTGAGCGGCAACCTGCT 193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 417 GGGGCTGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 194 CGGGCTCCAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 477 GCGGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 254 GCGGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 313
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 537 CACTGAGGCTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 314 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 597 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 374 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 657 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 434 CCGGAGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 717 GGTGTAATTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 494 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 777 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 554 CCGGAGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 837 CACGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 896
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 614 CACGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 897 CTACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 674 CTACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 957 CTGGGT 962
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 734 CTGGGT 739
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 10
US-10-437-963-99601

; Sequence 99601, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 99601
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_97398C.1
US-10-437-963-99601

Query Match 10.5%; Score 387.2; DB 8; Length 1764;
Best Local Similarity 77.2%; Pred. No. 1.1e-65;
Matches 505; Conservative 0; Mismatches 128; Indels 21; Gaps 2;

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QY 309 GTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 37 GTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 93
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 369 GCTGAACAAGGAGGAGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 94 GCTGAACAAGGAGGAGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 153
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 429 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 154 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 489 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 214 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 273
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 549 CAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 274 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 609 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 334 CCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 393
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 669 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 394 CAGC-----GAGCCTTCTACCCGAGGCAAGCTGCTGCTTCCA 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 729 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 436 GTTCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 789 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 496 CATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 849 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 556 CTTCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 909 CTACGTCATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 616 CTACGTCATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 11
US-10-437-963-81536

; Sequence 81536, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei

```

; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81536
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81052C.1
; US-10-437-963-81536

Query Match      10.5%; Score 385.4; DB 8; Length 1494;
Best Local Similarity 74.5%; Pred. No. 2.2e-65;
Matches 485; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 312 GGGCAGCGTGTGTCGCTGCGCGTACCAAGGGGAAACAGTCGCGCTGCGTGGCGGACTGCGT 371
DB 3 GGGGTGCGCGACCCGCGCGCGCGTACATGCGCGCCCAACCGCGGTGCGGAGTGGCT 62
QY 372 GAACAAGGGGAGAACAGCGCTGGAGAGCTGTGTGCGCGAGCGCTGTGGGGCTGCAGAGCGT 431
DB 63 GAACAAGGGGAGAACAGCGGTGGAGAGCTGTGTGCGCGAGCGCTGTGTGGGCTGCAGAGCGT 122
QY 432 GCGCGGCTGTGTGTGCTGTACAGCGCGCGTGTGTAAGAAAGAGTGGGGCTGTAACCTCGG 491
DB 123 GCGTGGGCTGTGTGTGCTGTACAGCGAGCATGTGAAGAAAGAGTGGGGCTGTAACCTCGG 182
QY 492 GTTCATGAGGCTTACAGCGCTTCCGCGCGGTGTGATCTGTGCGGTACCTGAGCGTACAA 551
DB 183 CTTCATGAGGCTTACAGCGGTACAGCGCTACATGTGTGGTGTGTGGCTTCCG 242
QY 552 CATGTGCTTGGGAGAGAGCTCTCCCGATCTGTGGGAGAGCGCGCGCGCTGAGACA 611
DB 243 CATGTGCTTGGGAGAGAGCTCTCCCGATCTGTGGGAGAGCGCGCGCGCTGAGACA 302
QY 612 GGGGCTCTGTGTGCGCGCGCGCGCGTCCGCGAGCGTCACTACCGCGCGAGCGGAG 671
DB 303 GGGGCTCTGTGTGCGCGCGCGCGCGTCCGCGAGCGGCACTACCGGAGAGAGCGGCGC 362
QY 672 CGTGAAGAGCGCGCGCGTGGAGCGCGTGTACCGGATGCGAGCGGTGTACTTCCAGTG 731
DB 363 CGTGAAGAGCGCGCGCGTGGAGCGCGTGTGTACCGGAGAGCGGTGTGTCTTCCAGTG 422
QY 732 CGTGTGCGCGCGCATACCTCATCTCGTCCGCGCTCTCTGCGCGCATGAGCTT 791
DB 423 CGAGGCTCGCGCGCATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482
QY 792 CCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
DB 483 CAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 542
QY 852 CTCCTCTGTGGGAGCGGCTTCTCTTTCACACTGGGCGTGTACACTGACACTGCGGCGGCTA 911
DB 543 CAGCCTCTGTGGGAGCGGCTTCTCTTTCACAGTGGGCGTGTACACTGACACTGCGGCGGATA 602
QY 912 CGTCAATCAAGTCTCGCGCGGAGTCCGCGGCTTACCGCGGCTTACTGGGT 962
DB 603 CGTCAATCAAGTCTCTCTCGCGGAGTCCGCGGCTTACCGCGGCTTACTGGGT 653

RESULT 12
US-10-437-963-86014
; Sequence 86014, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 86014
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85096C.1
; US-10-437-963-86014

Query Match      10.5%; Score 385.4; DB 8; Length 1494;
Best Local Similarity 74.5%; Pred. No. 2.2e-65;
Matches 485; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 312 GGGCAGCGTGTGTCGCTGCGCGTACCAAGGGGAAACAGTCGCGCTGCGTGGCGGACTGCGT 371
DB 3 GGGGTGCGCGACCCGCGCGCGCGTACATGCGCGCCCAACCGCGGTGCGGAGTGGCT 62
QY 372 GAACAAGGGGAGAACAGCGCTGGAGAGCTGTGTGCGCGAGCGCTGTGGGGCTGCAGAGCGT 431
DB 63 GAACAAGGGGAGAACAGCGGTGGAGAGCTGTGTGCGCGAGCGCTGTGTGGGCTGCAGAGCGT 122
QY 432 GCGCGGCTGTGTGTGCTGTACAGCGCGCGTGTGTAAGAAAGAGTGGGGCTGTAACCTCGG 491
DB 123 GCGTGGGCTGTGTGTGCTGTACAGCGAGCATGTGAAGAAAGAGTGGGGCTGTAACCTCGG 182
QY 492 GTTCATGAGGCTTACAGCGCTTCCGCGCGGTGTGATCTGTGCGGTACCTGAGCGTACAA 551
DB 183 CTTCATGAGGCTTACAGCGGTACAGCGCTACATGTGTGGTGTGTGGCTTCCG 242
QY 552 CATGTGCTTGGGAGAGAGCTCTCCCGATCTGTGGGAGAGCGCGCGCGCTGAGACA 611
DB 243 CATGTGCTTGGGAGAGAGCTCTCCCGATCTGTGGGAGAGCGCGCGCGCTGAGACA 302
QY 612 GGGGCTCTGTGTGCGCGCGCGCGCGTCCGCGAGCGGCACTACCGGAGAGAGCGGCGC 671
DB 303 GGGGCTCTGTGTGCGCGCGCGCGCGTCCGCGAGCGGCACTACCGGAGAGAGCGGCGC 362
QY 672 CGTGAAGAGCGCGCGCGTGGAGCGCGTGTGTACCGGATGCGAGCGGTGTACTTCCAGTG 731
DB 363 CGTGAAGAGCGCGCGCGTGGAGCGCGTGTGTACCGGAGAGCGGTGTGTCTTCCAGTG 422
QY 732 CGTGTGCGCGCGCATACCTCATCTCGTCCGCGCTCTCTGCGCGCATGAGCTT 791
DB 423 CGAGGCTCGCGCGCATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482
QY 792 CCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
DB 483 CAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 542
QY 852 CTCCTCTGTGGGAGCGGCTTCTCTTTCACACTGGGCGTGTACACTGACACTGCGGCGGCTA 911
DB 543 CAGCCTCTGTGGGAGCGGCTTCTCTTTCACAGTGGGCGTGTACACTGACACTGCGGCGGATA 602
QY 912 CGTCAATCAAGTCTCGCGCGGAGTCCGCGGCTTACCGCGGCTTACTGGGT 962
DB 603 CGTCAATCAAGTCTCTCTCGCGGAGTCCGCGGCTTACCGCGGCTTACTGGGT 653

RESULT 13
US-10-767-701-3848
; Sequence 3848, Application US/10767701
; Publication No. US20040172684A1
```

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 3848
LENGTH: 623
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS67017_1
US-10-767-701-3848

Query Match 10.2%; Score 376.4; DB 8; Length 623;
Best Local Similarity 82.8%; Pred. No. 8,3e-64;
Matches 457; Conservative 0; Mismatches 86; Indels 9; Gaps 2;

QY 289 TCAGCGACGAGATGTCGTCTGCGGACGATGTCCTGCGCTGACCGAGGGAACAGC 348
DB 78 TCGTCGGCAACTAACATGGCGTCGTCCGGAGAGATCCACTGCGTACAG-----ACG 131
QY 349 TCGGCGTCGTCGTCGCGACCTGCTGAACAAAGGGAGAACGCTGGGACCTGGTGGCGCG 408
DB 132 ACGGGACGCTCCCGCACTGCGCTGAACAAAGGCGAACAGCTGGGACGCTGAACGCGGCG 191
QY 409 ACGCTGTGGGCTGTCGAGAGCGTCGCGGCTGTTGTTGCTGTGAACGCGCGCTGTGAAG 468
DB 192 ACGCTGTGGGCTGTCGAGAGCTTCCCTGCGCTGTGTGTCTCTACGCGCGCGCTGTGAAG 251
QY 469 AAGAAATGGGCGGATGAATCGGCGTTCAATGCGCTTACGCGCTTCCGCGCGCTGTGATC 528
DB 252 AAGAAATGGGCGGATGAATCGGCGTTCAATGCGCTTACGCGCTTCCGCGCGCTGTGATC 311
QY 529 TCGTGGGTCACTGGGCGGTGAACAAATGTCTTCCGCGGAGAAAGCTCTCCGATCTGGGG 588
DB 312 TCGTGGGTCACTGGGCGGTGAACAAATGTCTTCCGCGGAGAAAGCTCTCCGATCTGGGG 371
QY 589 AAGGCGCGGCGCGGCTGAGACCAAGGCGCTCTGTCGCGCGCGCGCGCTGCGCGGAGC 648
DB 312 AAGGCGCGGCGCGGCTGAGACCAAGGCGCTCTGTCGCGCGCGCGCGCTGCGCGGAGC 431
QY 649 GTCACTACCGCGCGACG---GCAACGTGAGAACGCGCGCGGTGAGCGCGCTGTACCGG 705
DB 432 GTCACTACTTTCGCCAACGGAGACCATCGAAGCGCGCGCGCGGACACTGTATCCCG 491
QY 706 ATGGCGACGCTGTGTACTTCCAGTGGGTGTTGCGCGCATACCTCATCTCTCGTGGCG 765
DB 492 ATGGCGACGCTGTGTACTTCCAGTGGGTGTTGCGCGCATACCGTGTATCTCTGTGGCG 551
QY 766 GCGTCCCTCTCGGCGCGCATGAGCTTCTGCGCTGTGATCTTCTCCGCTGTGGCTC 825
DB 552 GCGTCCCTCTCGGCGCGCATGAGCTTCTGCGCGCTGTGATCTTCTCTGCGCTGTGGCTC 611
QY 826 ACCCTTCTCTAC 837
DB 612 ACCCTTCTCTAC 623

RESULT 14
US-10-425-115-177223

; Sequence 177223, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 177223
LENGTH: 1920
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_93216C.1
US-10-425-115-177223

Query Match 10.2%; Score 375.2; DB 9; Length 1920;
Best Local Similarity 77.7%; Pred. No. 2,6e-63;
Matches 474; Conservative 0; Mismatches 118; Indels 18; Gaps 1;

QY 353 CGTCGTCGCGGACGCTGTGAACAAAGGGAGCAACGCGTGGCACTGTGCGCGGACGC 412
DB 328 CGGCGTCGCGGAGTGGCTTAACAAAGGCGCAACAGCTGGCAGCTGACGCGCGGACGC 387
QY 413 TGGTGGGCTGCAAGCGTTCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 472
DB 388 TGGTGGGCTGCAAGCGTTCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 447
QY 473 AGTGGCGGATGAATCGGCGTTCAATGCGCTTACGCGCTTCCGCGCGCGCTGTGATCTGCT 532
DB 448 AGTGGCGGATGAATCGGCGTTCAATGCGCTTACGCGCTTCCGCGCGCGCTGTGATCTGCT 507
QY 533 GGGTCACTGGGCGGTGAACATGTCTTCCGCGGAGAACCTCTCCGATCTGGGGGAGG 592
DB 508 GGGTCACTGGGCGGTTCGCAATGGCGTTCCGCGGAGCGGCTGCTCCGTTCTGGGGCAAG 567
QY 593 CGGCGCGCGCTGTGAACAGGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
DB 568 CGGCGCGCGCTTCCGCGGAGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 627
QY 653 ACTACGCGCGGACGCGGACGTCGAGACGCGCGCGGTCGAGACCGCTGTACCGGATGCGA 712
DB 628 ACGGCGCGGACCGCGCGCAC-----GAGCGCTGTATCCGAGGCGCA 669
QY 713 CGGTGTGTACTTCCAGTGGGTGTTGCGCGCGCATACCTTCATCTGTGCGCGCTGCC 772
DB 670 CGCTTGTGTGTGTTCAGTTCGAGTTGCGCGCGCATACCTTCGAGTGTCTTGGCGCGCTCG 729
QY 773 TCGTGGCGGATGAGCTTCTCGCGCTGAGATGTTGTGTCGCGCTTGGCTCACTTCT 832
DB 720 TCGTGGCGGATGAGCTTCTCGCGCTGAGATGTTGTGTCGCGCTTGGCTCACTTCT 789
QY 833 CCTACACGTCGCGCGCTTCTCTCTGCGCGCGCGCGCTTCTCTTCACTGGGCGTCA 892
DB 790 CCTACACGTCGCGCGCTTCTCTCTGAGCATCTGGGCGCGCGCTTCTCTTCACTGGGCGTCA 849
QY 893 TCGACTACTGCGCGGCTACGTCATCAAGTCTCCGCGGACGCGCGCTTCACTGCGCG 952
DB 850 TCGACTACTGCGCGGATACGTCATCAAGTCTCTCGGCGCATCGCGGCTTCACTGCGCG 909
QY 953 CTTACTGGGT 962
DB 910 CATACTGGGT 919

RESULT 15
US-10-437-963-47680

; Sequence 47680, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 47680
LENGTH: 1443
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_50425C.1
US-10-437-963-47680

Query Match 10.2%; Score 374.2; DB 8; Length 1443;
Best Local Similarity 75.3%; Pred. No. 3,5e-63;
Matches 466; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 344 ACACTGCGCGCTGCGTGGCGGACTGGCTGAACAAGGGGGAACAAGCGCTGGCACTGGTG 403
DB 32 AGACCACTCCGTATCGCCAGACTGGCTGAACAAGGGGGAACAAGCGATGGCAATGACAT 91
QY 404 CGGCGACGCTGGTGGGGCTGCAAGGCTGCCGGCTTGGTGGCTGTACGCGGGGCTGG 463
DB 92 CGGCGACCTCGCTGGGCTGCAAGGATGCGAGGGCTGGTATCTGTACGCGGACATTG 151
QY 464 TGAAGAAGAAGTGGGCGGTGAACCTCGGCGCTTCATGGCGCTTACGCGCTTCCGCGCTGT 523
DB 152 TCAAGAAGAAGTGGGCTATCAACTCGGCGCTTCATGGCGCTTATGCTTGGCTGTCT 211
QY 524 GGATCTGTGGGTCACTGGGCGGTACAAATGCTTGGGGGAAGCTCTCCGATCT 583
DB 212 GGATCTGTGGGTGCTGGGCAATACAAATGCTTGGGCGACCGCTCTGCAATCT 271
QY 584 GGGGGAAGCGCGCGCGCTGGACCAAGGCTCTCTCGTGGGCGCGCGCGCTGGCCCG 643
DB 272 GGGGTAAGGCAAGCGCGCGCTGGGCAAGCTTCTCTGGGCGCAATGAGCTCACTG 331
QY 644 CGACGCTCACTACCGCGCGCAAGCGGCGGTGAGACGCGCGCTGTACC 703
DB 332 CTACCGCTATTCGCTTACCAATGGGTCAAGGCGCCCATGCTCAAGCGCTGTACC 391
QY 704 CGATGGCGAAGGTGTGTACTTCCAGTGCCTGTTCGCGCGCATCACCTCATCTGCTG 763
DB 392 CAGTGGCAACAGTGTACTTCCAGTGCATGTTTGGAGCATCACCATCATCATCTG 451
QY 764 CGGCTCCCTCTCGGCGCGCATAGCTTCTCGCTGGATGATCTTCTGCTCGGCTTGGC 823
DB 452 CAGGCTCACTGCTGGGCGCATGAACATCAAGGCGTGAATGCGCTTGTGCGCTTGA 511
QY 824 TCACCTTCTCTTACACGATCGGCGCTTCCCTTGGGGCGGCGGCTTCTCTTCACT 883
DB 512 TCACCTTCTCTTACACGATCGGCTTCCCTTGGGGCGGCTTCTCTTCACT 571
QY 884 GGGGCGTCACTGACTGCGCGGCTACGCTACATCAAGTCTCGCGCGCATGCGCGCT 943
DB 572 GGGGTGTCATAGACTCTGATGGCTATGATCATCATCTCTTTCGCGCATGCGAGGC 631
QY 944 TCACGCGCGCTTACTGGGT 962
DB 632 TCACGCTGCTACTGGGT 650

Search completed: July 23, 2006, 21:30:36
Job time : 4207 secs

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QY 121 TATGTTGAATAGAGCAGAGGAGTACAGTACAGGCTTACTAGCCAGAGTCAAAAT 180
DB 121 TATGTTGAAATAGAGCAGAGGAGTACAGTACAGGCTTACTAGCCAGAGTCAAAAT 180
QY 181 GGTATATCATGAGCCACTGAGCAATGCACTCTCTATATATAGCTCCCTTAATAGAC 240
DB 181 GGTATATCATGAGCCACTGAGCAATGCACTCTCTATATATAGCTCCCTTAATAGAC 240
QY 241 TAGCTAGGATACCAAAAGAAAGGCATACCAAGCTTAGTGTGTGATACAGAGCAAG 300
DB 241 TAGCTAGGATACCAAAAGAAAGGCATACCAAGCTTAGTGTGTGATACAGAGCAAG 300
QY 301 ATGTGCTGTGCGGCGAGCGGTGCGGCTGAGGCTGAGGAGGAAACGTCGCGTGGG 360
DB 301 ATGTGCTGTGCGGCGAGCGGTGCGGCTGAGGCTGAGGAGGAAACGTCGCGTGGG 360
QY 361 GCGGACTGCTGAACAAAGGGGAGCAACGCGTGGCAGCTGTGGCGGCGACGCTGTGGG 420
DB 361 GCGGACTGCTGAACAAAGGGGAGCAACGCGTGGCAGCTGTGGCGGCGACGCTGTGGG 420
QY 421 CTGCAAGAGCTGCCGGGCTTGTGTGTGTGTAAGCGGCGGTGTGAAGAAAGTGGGCG 480
DB 421 CTGCAAGAGCTGCCGGGCTTGTGTGTGTGTAAGCGGCGGTGTGAAGAAAGTGGGCG 480
QY 481 GGAAGCTGCGCGTCAATGGGCGCTTACGCGCTTCCGCGCGGTGTGATCTGTGGGTCAAC 540
DB 481 GGAAGCTGCGCGTCAATGGGCGCTTACGCGCTTCCGCGCGGTGTGATCTGTGGGTCAAC 540
QY 541 TGGGCGTACAAATGTCGTTCCGGGGAGAAAGCTCTCCGATCTGGGGGAAAGGCGGGCGG 600
DB 541 TGGGCGTACAAATGTCGTTCCGGGGAGAAAGCTCTCCGATCTGGGGGAAAGGCGGGCGG 600
QY 601 GCGCTGAGCAAGGGCTCTCTCGTCCGCGCGCGCGCTGCGCGGCTCACTACCGC 660
DB 601 GCGCTGAGCAAGGGCTCTCTCGTCCGCGCGCGCTGCGCGGCTCACTACCGC 660
QY 661 GCGGACGCGAGGCTGGAGACGCGCGGCGGTGAGACGCTGACCCGATGGAGAGGTGGTG 720
DB 661 GCGGACGCGAGGCTGGAGACGCGCGGCGGTGAGACGCTGACCCGATGGAGAGGTGGTG 720
QY 721 TACTTCCAGTGGGTGTCGCGCGCATCACTCATCTGTCGCGCTCCCTCGTCCGCGC 780
DB 721 TACTTCCAGTGGGTGTCGCGCGCATCACTCATCTGTCGCGCTCCCTCGTCCGCGC 780
QY 781 CGCATGAGCTTCTCGCTGAGTATCTTCCGCTCGCTCGCTCACTTCTCTACAC 840
DB 781 CGCATGAGCTTCTCGCTGAGTATCTTCCGCTCGCTCGCTCACTTCTCTACAC 840
QY 841 GTGCGGCGCTTCCGCTGAGGCGGCGGCTTCTGCACTGGGCGGTCACTGACCTAC 900
DB 841 GTGCGGCGCTTCCGCTGAGGCGGCGGCTTCTGCACTGGGCGGTCACTGACCTAC 900
QY 901 TCGCGGCGGTACGTATCCACGTCCTCGCGGATGCGCGGCTTCACTCGCGCTTACTGG 960
DB 901 TCGCGGCGGTACGTATCCACGTCCTCGCGGATGCGCGGCTTCACTCGCGCTTACTGG 960
QY 961 GTCCGCTACACAGCTCATCTTTTGTCTTATCTTACTCATGCGCAGATTTAAAT 1020
DB 961 GTCCGCTACACAGCTCATCTTTTGTCTTATCTTACTCATGCGCAGATTTAAAT 1020
QY 1021 TTTCAATCATAAATTTAAAGCTAATTTTAAAGTTTTCATGAGTTATTTTTCATC 1080
DB 1021 TTTCAATCATAAATTTAAAGCTAATTTTAAAGTTTTCATGAGTTATTTTTCATC 1080
QY 1081 ATTTGTTTTAGTGCCTAAGAACAGTATATATAAGTTTATTCACAAATTAATTAATG 1140
DB 1081 ATTTGTTTTAGTGCCTAAGAACAGTATATATAAGTTTATTCACAAATTAATTAATG 1140
QY 1141 TTCAAGACTAAGCTAAACATAGTACTCACTTTTGGCGCGCGCGCAGAGTGCAGTAG 1200
DB 1141 TTCAAGACTAAGCTAAACATAGTACTCACTTTTGGCGCGCGCGCAGAGTGCAGTAG 1200

QY 1201 CTCTGACAAGTGTACATATCATATGTTGGCTGGCAGAGTGGGGCCAGAGGCGCAGAGAGAC 1260
DB 1201 CTCTGACAAGTGTACATATCATATGTTGGCTGGCAGAGTGGGGCCAGAGGCGCAGAGAGAC 1260
QY 1261 AAGGAGAGGTTCCCGCGCAACATATACGTTTCACTGCTGACGCGGGGCGAGGCTGTGG 1320
DB 1261 AAGGAGAGGTTCCCGCGCAACATATACGTTTCACTGCTGACGCGGGGCGAGGCTGTGG 1320
QY 1321 ATGGGGTGGGAGGGTTTCAAGCGCGCGGTCGTAACGCGCGCACTCGTGGCCCTTAATG 1380
DB 1321 ATGGGGTGGGAGGGTTTCAAGCGCGCGGTCGTAACGCGCGCACTCGTGGCCCTTAATG 1380
QY 1381 GCGGTCTCAACACCAATCATGACCGCACGACCTCATGCTGTGACATGCTCTGAC 1440
DB 1381 GCGGTCTCAACACCAATCATGACCGCACGACCTCATGCTGTGACATGCTCTGAC 1440
QY 1441 GTCATCTTCTTCAGAGACCTCGTGTGCGCGCGCTGACAGGCGATATCACCGGCTC 1500
DB 1441 GTCATCTTCTTCAGAGACCTCGTGTGCGCGCGCTGACAGGCGATATCACCGGCTC 1500
QY 1501 GTTTCGATCACCCCGCGTGCAGGTACGTAATCATCACTACACGAGAAACGAAAGCCTT 1560
DB 1501 GTTTCGATCACCCCGCGTGCAGGTACGTAATCATCACTACACGAGAAACGAAAGCCTT 1560
QY 1561 ATTAATTAAGTATTAAGTAAATACTTAAAGTAAATTAATGATATTTTTCTTGA 1620
DB 1561 ATTAATTAAGTATTAAGTAAATACTTAAAGTAAATTAATGATATTTTTCTTGA 1620
QY 1621 AAAATTCGCGAAATATACATTTAGTAAATTTTGCATATGTTGTAGAAAGAGAG 1680
DB 1621 AAAATTCGCGAAATATACATTTAGTAAATTTTGCATATGTTGTAGAAAGAGAG 1680
QY 1681 TTGAAGTTGAAAAAATGAGTACGGAACACAGCCTTATTAATGAATGTTGTAGT 1740
DB 1681 TTGAAGTTGAAAAAATGAGTACGGAACACAGCCTTATTAATGAATGTTGTAGT 1740
QY 1741 ACTTAATTAATCTTTGGAGTGAATGATACGTAATGAGTGGCGCGTGAACAGCGCGGA 1800
DB 1741 ACTTAATTAATCTTTGGAGTGAATGATACGTAATGAGTGGCGCGTGAACAGCGCGGA 1800
QY 1801 TCGATTTCTTAATTAAGTATTAATCCCGGTTTGCAATTAATGATCTTCCCGCCAG 1860
DB 1801 TCGATTTCTTAATTAAGTATTAATCCCGGTTTGCAATTAATGATCTTCCCGCCAG 1860
QY 1861 TTGTTTACCTTTGAATCTTAACTGTGCGGTGCGCAACATACAGAGGTGGTTACC 1920
DB 1861 TTGTTTACCTTTGAATCTTAACTGTGCGGTGCGCAACATACAGAGGTGGTTACC 1920
QY 1921 TTGCTGCGCAATTAATGCAATTTTCCCGTAGATTAACGCGTTTACATTTTGTGGCA 1980
DB 1921 TTGCTGCGCAATTAATGCAATTTTCCCGTAGATTAACGCGTTTACATTTTGTGGCA 1980
QY 1981 CTAAATTAAGCAGCAGCAGCACTGATTCATATCTCTCTCATCTCTTGTAGTGG 2040
DB 1981 CTAAATTAAGCAGCAGCAGCACTGATTCATATCTCTCTCATCTCTTGTAGTGG 2040
QY 2041 AAGAGTGTAAAGTTTTCATCTTTTCAAGTTGTGATGATGATGATGATGATGATGAT 2100
DB 2041 AAGAGTGTAAAGTTTTCATCTTTTCAAGTTGTGATGATGATGATGATGATGATGAT 2100
QY 2101 TTAATTTCCGCTCACTAGTCACTACAGTACCTAATGTGAACAAATATCAAGCTCATCGG 2160
DB 2101 TTAATTTCCGCTCACTAGTCACTACAGTACCTAATGTGAACAAATATCAAGCTCATCGG 2160
QY 2161 AATCTAGGTTGATGATCATATATTTTCCGCAACAGAGATCTTATTTGTGCTTC 2220
DB 2161 AATCTAGGTTGATGATCATATATTTTCCGCAACAGAGATCTTATTTGTGCTTC 2220
QY 2221 GTGCTTAATGTAATGAGAAATCATCATCTAGTGTGATGATGATGATGATGATGATGAT 2280
DB 2221 GTGCTTAATGTAATGAGAAATCATCATCTAGTGTGATGATGATGATGATGATGATGAT 2280
QY 2281 TCTGAAGCTGCAATTTGTTTTTTCTGAGTTTTTCTGTAACGAGAGCCAGAGAAAG 2340

Db	2281	TCGAAACTGCCAATTGTTTTTTTCTGAGTTTTTCTTGACGAAAGCAGCAAGAAAG	2340
Qy	2341	CACACTGAAAATGAAAGTAGAATATTTTACAGCCTCCATTCCGTCCGTGACTTCGTTCA	2400
Db	2341	CACACTGAAAATGAAAGTAGAATATTTTACAGCCTCCATTCCGTCCGTGACTTCGTTCA	2400
Qy	2401	AAGCTATATTTACGGGGCGAGATGAGACTACAGTACTCATATGCAATTTGCTGATGATCA	2460
Db	2401	AAGCTATATTTACGGGGCGAGATGAGACTACAGTACTCATATGCAATTTGCTGATGATCA	2460
Qy	2461	GGCACTGTCACTGCTATCGCAAGAGATCCGTGCTCTTATTTATGACACATGACACACC	2520
Db	2461	GGCACTGTCACTGCTATCGCAAGAGATCCGTGCTCTTATTTATGACACATGACACACC	2520
Qy	2521	TACACCCCTTATCATTTATTTGTTTTAGATTTGTGGTATTAATACAGATTTCAATAGA	2580
Db	2521	TACACCCCTTATCATTTATTTGTTTTAGATTTGTGGTATTAATACAGATTTCAATAGA	2580
Qy	2581	GCATPAACATTATGATTTTTCTTTTCCTGTAACAACAAGATCTCAATPAATATATCTC	2640
Db	2581	GCATPAACATTATGATTTTTCTTTTCCTGTAACAACAAGATCTCAATPAATATATCTC	2640
Qy	2641	TTTTTCGATGAAAACATPAATGACTTTGACAGATTTCTATCTGTCCTAAATPAATT	2700
Db	2641	TTTTTCGATGAAAACATPAATGACTTTGACAGATTTCTATCTGTCCTAAATPAATT	2700
Qy	2701	CATTTTTTAAATTTCTATGTCGAACATTTGATCATCCGTTTATTTTAAAAAATATATAT	2760
Db	2701	CATTTTTTAAATTTCTATGTCGAACATTTGATCATCCGTTTATTTTAAAAAATATATAT	2760
Qy	2761	TTTTTATPAATAAGTCATACATPAATAAGATTTATTTATTTTATTTATCTAATPAACAATPAAG	2820
Db	2761	TTTTTATPAATAAGTCATACATPAATAAGATTTATTTATTTTATTTATCTAATPAACAATPAAG	2820
Qy	2821	AATTTTAACTATTTAAAAATTAATAATPAAGCGAAGATCAAAAGGTATGATGGTATGTG	2880
Db	2821	AATTTTAACTATTTAAAAATTAATAATPAAGCGAAGATCAAAAGGTATGATGGTATGTG	2880
Qy	2881	CAGGGGTGTCACAGGGGTGGCGCGCTGTGATAGGGGGTCTCGCCGGACGATCCCGT	2940
Db	2881	CAGGGGTGTCACAGGGGTGGCGCGCTGTGATAGGGGGTCTCGCCGGACGATCCCGT	2940
Qy	2941	GGTACACCATGATGATCTCTCCACAAGCGCTCCAGAGATCTCAGCGGTGACACACACC	3000
Db	2941	GGTACACCATGATGATCTCTCCACAAGCGCTCCAGAGATCTCAGCGGTGACACACACC	3000
Qy	3001	TGCGGCTTTTCCACACCCACCGCGCTCGCCGCTCTCGGGGCTCTTCCACCGGCTCT	3060
Db	3001	TGCGGCTTTTCCACACCCACCGCGCTCGCCGCTCTCGGGGCTCTTCCACCGGCTCT	3060
Qy	3061	TGCGGAGCGCACCCCTTCGCAACCTCTCTCCCGGTGGCGGACTCCCGGGGCGCTTCT	3120
Db	3061	TGCGGAGCGCACCCCTTCGCAACCTCTCTCCCGGTGGCGGACTCCCGGGGCGCTTCT	3120
Qy	3121	ACGGCGGCGCGCGCGCCAGTTTCGCAAGCAGATCGCGCGGCTCTTTCGTGCTGC	3180
Db	3121	ACGGCGGCGCGCGCGCCAGTTTCGCAAGCAGATCGCGCGGCTCTTTCGTGCTGC	3180
Qy	3181	CCTGGAACGTGCTGCTCACTTCCTCATCTGCTTCGTCATCACTCTTGGTCCGCTTC	3240
Db	3181	CCTGGAACGTGCTGCTCACTTCCTCATCTGCTTCGTCATCACTCTTGGTCCGCTTC	3240
Qy	3241	GCATGCCCGAAGCAAGCTCGAGGTGGCGGAGCAAGCGCTCAACGCGGAGGAGGCTAAG	3300
Db	3241	GCATGCCCGAAGCAAGCTCGAGGTGGCGGAGCAAGCGCTCAACGCGGAGGAGGCTAAG	3300
Qy	3301	CGCTCTGGGGCGACGGCGAGATGTACAGAGTACCAACACAGGCTCCGACCGCGCGTTG	3360
Db	3301	CGCTCTGGGGCGACGGCGAGATGTACAGAGTACCAACACAGGCTCCGACCGCGCGTTG	3360
Qy	3361	CCCCCGTCGTGATGATGATCACTTAAATTCATGTGCTGTCACTGATGAAAACCTC	3420
Db	3361	CCCCCGTCGTGATGATGATCACTTAAATTCATGTGCTGTCACTGATGAAAACCTC	3420

Db	3361	CCCCCGTCGTCGATGATCGATCACTTAAATGCGATGCGTCGTCACCTCGATGAAAACCTC	3420
Qy	3421	AAGAAATTCATPACACACAGAAATTAATACTACGCTTGGCTCTCTACTCGGTTAATTATGAA	3480
Db	3421	AAGAAATTCATPACACACAGAAATTAATACTACGCTTGGCTCTCTACTCGGTTAATTATGAA	3480
Qy	3481	AATCTATGTCMACTTTTACGTCGTAATTTAAACGCGCGCGTCGAGTATGGCAATTGCAC	3540
Db	3481	AATCTATGTCMACTTTTACGTCGTAATTTAAACGCGCGCGTCGAGTATGGCAATTGCAC	3540
Qy	3541	TTGAGATTCAGGGGAGTCGCGTCTGATTTTGTAGTTGTAAAAATGTATACGTAG	3600
Db	3541	TTGAGATTCAGGGGAGTCGCGTCTGATTTTGTAGTTGTAAAAATGTATACGTAG	3600
Qy	3601	TTTTGTATCCTTACTGATCTGAATGAACACACAGTGAATTTATTTTGTAAATTAG	3660
Db	3601	TTTTGTATCCTTACTGATCTGAATGAACACACAGTGAATTTATTTTGTAAATTAG	3660
Qy	3661	CTCCATATTTTCCAAA 3677	
Db	3661	CTCCATATTTTCCAAA 3677	

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RESULT 2
US-10-449-902-24969
; Sequence 24969, Application US/10449902
; Publication NO. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiol
; APPLICANT: Bio-oriented Technology Resea
; APPLICANT: The Institute of Physical and
; APPLICANT: Foundation for Advancement o
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA
; FILE REFERENCE: MOA-A020511-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-385870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24969
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK100411
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24969

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Query Match	20.3%	Score 746.4	DB 6	Length 1790
Best Local Similarity	97.7%	Pred. No. 1.9e-133		
Matches 780	0	Mismatches 11	Indels 7	Gaps 2

[illegible]

Db 1236 CTACGCGGCGCGCGGCGGCCCACTGTCGGAAGAGATCGCCGGTGCCCTTCGTGCT 1295
Qy 3179 CGCCTGGAACGTCGTCTACCTCCCTCATCTGCTCGGCATCAACCTCTGTCGCCGT 3238
Db 1296 CGCCTGGAACGTCGTCTACCTCCCTCATCTGCTCGGCATCAACCTCTGTCGCCGT 1355
Qy 3239 CGCAGTCCCGGACGACAAAGCTCGAGTCGCGACGACGCGCTCCACGCGGAGAGAGCTTA 3298
Db 1356 CGCAGTCCCGGACGACAAAGCTCGAGTCGCGACGACGCGCTCCACGCGGAGAGAGCTTA 1415
Qy 3299 CGCGCTCTGGGGCGACGCGGAGATGTACGACGTCACCAAGCAGGCTCCGACGCCCGCT 3358
Db 1416 CGCGCTCTGGGGCGACGCGGAGATGTACGACGTCACCAAGCAGGCTCCGACGCCCGCT 1475
Qy 3359 TCGCCCGCTGTCGTATGATCATTAATTGATGTGCTGTACCTGATGAAGACC 3418
Db 1476 TCGCGCCGCTGTCGTATGATCATTAATTGATGTGCTGTACCTGATGAAGACC 1531
Qy 3419 TCAAGAAATTCATACACAGAAATTAATACGATGCTGCTCTACTGTTAATTATG 3478
Db 1532 TCAAGAAATTCATACACAGAAATTAATACGATGCTGCTCTACTGTTAATTATG 1591
Qy 3479 AAAATCTATGTCAGATTTTACGTGTATTTAAACGCGCGCTGTGAG---TTAGGCATT 3535
Db 1592 AAAATCTATGTCAGATTTTACGTGTATTTAAACGCGCGCTGTGAGTTTAAAGTATT 1651
Qy 3536 GCACCTTTCAGATTCAGGGGAGTCCGCTCTGTATTTTGTAGTTGTTAAAAATGATA 3595
Db 1652 GCACCTTTCAGATTCAGGGGAGTCCGCTCTGTATTTTGTAGTTGTTAAAAATGATA 1711
Qy 3596 CGTAGTTTGTATTCCTTACTGATCTGAATGAACAAGATGTAATTAATTATTTGTTAA 3655
Db 1712 CGTAGTTTGTATTCCTTACTGATCTGAATGAACAAGATGTAATTAATTATTTGTTAA 1771
Qy 3656 TTAAGCTCCATATTTTCC 3673
Db 1772 TTAAGCTCCATATTTTCC 1789

RESULT 3
US-10-449-902-18930
; Sequence 18930, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18930
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: *Oryza sativa*
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK069311
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18930

Query Match 20.0%; Score 733.6; DB 6; Length 1441;
Best Local Similarity 98.0%; Pred. No. 4,9e-131;
Matches 766; Conservative 0; Mismatches 9; Indels 7; Gaps 2;
Qy 2879 TCACGCGGTCGTGCAAGGGTGGCGCGCTGTGATGGGGTGTCTGCCGCGAGCATCC 2938
|||||

Db 684 TGCAGGGGTGTGTGACAGGGGTGGCGCGCTGTGTATGCGGGGTGTCTCCGCGGAGCATCC 723
Qy 2939 GTGTGACACCATGATGATCTTCAACAGGCTCCAAAGATCTCTGACAGCGGTCGACGAC 2998
Db 724 GTGTGACACCATGATGATCTTCAACAGGCTCCAAAGATCTCTGACAGCGGTCGACGAC 783
Qy 2999 CCTCGGCTCTTTCACACCCACCGGCTGTGCGGCTCTCTCGGAGGCTCTCTACCGGCT 3058
Db 784 CCTCGGCTCTTTCACACCCACCGGCTGTGCGGCTCTCTCGGAGGCTCTCTACCGGCT 843
Qy 3059 CTTGCGGAGCCACCTCTCTCAACCTTCTCTCCCGTCCCGCATCACTCCGAGGCGCTT 3118
Db 844 CTTGCGGAGCCACCTCTCTCAACCTTCTCTCCCGTCCCGCATCACTCCGAGGCGCTT 903
Qy 3119 CTACGCT 3178
Db 904 CTACGCT 963
Qy 3179 CGCCTGGAACGTCGTCTGTCACCTCCCTCATCTGCTCGGCATCAACCTCTGTCGCCGT 3238
Db 964 CGCCTGGAACGTCGTCTGTCACCTCCCTCATCTGCTCGGCATCAACCTCTGTCGCCGT 1023
Qy 3239 CGCAGTCCCGACGACCAAGCTCGAGTCTGAGTGGCGACGACCGCTCCACGCGAGGCGCTA 3298
Db 1024 CGCAGTCCCGACGACCAAGCTCGAGTCTGAGTGGCGACGACCGCTCCACGCGAGGCGCTA 1083
Qy 3299 CGCGCTCTGGGGCGACGCGCGGAGATGTACAGAGTCAACCAAGAGGCTCCGCGCGCT 3358
Db 1084 CGCGCTCTGGGGCGACGCGCGGAGATGTACAGAGTCAACCAAGAGGCTCCGCGCGCT 1143
Qy 3359 TCGCCCGCTGTCGTATGATCATTAATTGATGTGCTGTACCTGATGAAGACC 3418
Db 1144 TCGCGCGCTGTCGTATGATCATTAATTGATGTGCTGTACCTGATGAAGACC 1199
Qy 3419 TCAAGAAATTCATACACAGAAATTAATACGATGCTGTTGCTTACTGTTAATTATG 3478
Db 1200 TCAAGAAATTCATACACAGAAATTAATACGATGCTGTTGCTTACTGTTAATTATG 1259
Qy 3479 AAAATCTATGTCAGATTTTACGTGTATTTAAACGCGCGCTGTGAG---TTAGGCATT 3535
Db 1260 AAAATCTATGTCAGATTTTACGTGTATTTAAACGCGCGCTGTGAGTTTAAAGTATT 1319
Qy 3536 GCACCTTTCAGATTCAGGGGAGTCCGCTCTGTATTTTGTAGTTGTTAAAAATGATA 3595
Db 1320 GCACCTTTCAGATTCAGGGGAGTCCGCTCTGTATTTTGTAGTTGTTAAAAATGATA 1379
Qy 3596 CGTAGTTTGTATTCCTTACTGATCTGAATGAACAAGATGTAATTAATTATTTGTTAA 3655
Db 1380 CGTAGTTTGTATTCCTTACTGATCTGAATGAACAAGATGTAATTAATTATTTGTTAA 1439
Qy 3656 TT 3657
Db 1440 TT 1441

RESULT 4
US-10-713-648A-46
; Sequence 46, Application US/10713648A
; Publication No. US20060107344A1
; GENERAL INFORMATION:
; APPLICANT: POSCO
; APPLICANT: POSTECH
; APPLICANT: An, Gynheung
; APPLICANT: Ryu, Choong-Hwan
; APPLICANT: Han, Jong-Jin
; APPLICANT: Kang, Hong-Gyu
; APPLICANT: An, Kyungsok
; TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
; FILE REFERENCE: 2001-0-04USA
; CURRENT APPLICATION NUMBER: US/10/713,648A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/427,166

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? PRIOR FILING DATE: 2002-11-15
? NUMBER OF SEQ ID NOS: 83
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 46
? LENGTH: 1457
? TYPE: DNA
? ORGANISM: Oryza sativa
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (0)..(0)
? OTHER INFORMATION: line 1C-109-35 coding sequence
? US-10-713-648A-46

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Query Match	18.0%	Score 662;	DB 6;	Length 1437;
Best Local Similarity	99.3%	Pred. No. 2.6e-117;		
Matches 665;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

QY	301	ATGTCGTGTCGGGCGA	CGGTGGTGGCGCTGGGGGTAC	CAAGGGGAA	CACGTCCGGCTGGTGG	360
Db	1	ATGTCGTGTCGGGCGA	CGGTGGTGGTGCCTGGGGGTAC	CAAGGGGAA	CACGTCCGGCTGGTGG	60
QY	361	GCGGACTGGCTGAA	CAAGGGGGACA	CGCTGGGCA	CGCTGGTGGGG	420
Db	61	GCGGACTGGCTGAA	CAAGGGGGACA	CGCTGGGCA	CGCTGGTGGGG	120
QY	421	CTGCAAGACCGTGC	CGGGGCTTGGTGGTGGCTGTAC	CGGCGCGTGGTGAAGAA	AGTGGGGG	480
Db	121	CTGCAAGACCGTGC	CGGGGCTTGGTGGTGGCTGTAC	CGGCGCGTGGTGAAGAA	AGTGGGGG	180
QY	481	GTGAACCTGGGCGTTCAT	GGCGCTCTTACCGCTTC	CGCGCGTGGTGAATCTG	TGGGTAC	540
Db	181	GTGAACCTGGGCGTTCAT	GGCGCTCTTACCGCTTC	CGCGCGTGGTGAATCTG	TGGGTAC	240
QY	541	TGGGGGTACACAT	GTCTGTTGGGGGAGAAG	CTCTCCGATCTGGGGGAAAG	CGCGCGCG	600
Db	241	TGGGGGTACACAT	GTCTGTTGGGGGAGAAG	CTCTCCGATCTGGGGGAAAG	CGCGCGCG	300
QY	601	GCGCTGGACCAAGGG	CTCTCGTCCGGGCGCGCGCGCTCG	CGGCGA	CGGTACCTACCG	660
Db	301	GCGCTGGACCAAGGG	CTCTCGTCCGGGCGCGCGCGCTCG	CGGCGA	CGGTACCTACCG	360
QY	661	GCCGACGGCAGCGTGA	GAAGCGGCGGTGAGCGGCTGTAC	CCCGATGGCGA	CGGTGGTG	720
Db	361	GCCGACGGCAGCGTGA	GAAGCGGCGGTGAGCGGCTGTAC	CCCGATGGCGA	CGGTGGTG	420
QY	721	TACTTCCAGTGGGTTC	GGCGGCGCCATCA	CCCTCATCTGTGGCGGGCTCC	CTCCGGG	780
Db	421	TACTTCCAGTGGGTTC	GGCGGCGCCATCA	CCCTCATCTGTGGCGGGCTCC	CTCCGGG	480
QY	781	CGCATAGAGCTTC	CTGGCCTGATGTACTT	CGTCCCGGCTTGGGTCA	CTTCTCTTAC	840
Db	481	CGCATAGAGCTTC	CTGGCCTGATGTACTT	CGTCCCGGCTTGGGTCA	CTTCTCTTAC	540
QY	841	GTCGGCGGCTTCT	CCCTCTGGGGCGGCGGGCTTCT	TTTCACTGGGGCGTCA	TCACTAC	900
Db	541	GTCGGCGGCTTCT	CCCTCTGGGGCGGCGGGCTTCT	TTTCACTGGGGCGTCA	TCACTAC	600
QY	901	TGCGGCGGCTAC	GTATCCACGCTTCCGCGGCGAT	CGCGGCTTCA	CCGCGCTTACTG	960
Db	601	TGCGGCGGCTAC	GTATCCACGCTTCCGCGGCGAT	CGCGGCTTCA	CCGCGCTTACTG	660
QY	961	GTCCGCTACTA	970			
Db	661	GTGGGGCCAA	670			

RESULT 5
US-11-218-305-7343
; Sequence 7343, Application US/11218305
; Publication No. US2006014195A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McClaird, Paul L.

```

: APPLICANT: Tao, Nengsheng
: APPLICANT: Mu, Kunsheng
: TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
: TITLE OF INVENTION: Corn,
: FILE REFERENCE: 38-21 (53660)B
: CURRENT APPLICATION NUMBER: US/11/218,305
: CURRENT FILING DATE: 2005-09-01
: PRIOR APPLICATION NUMBER: US 60/606,880
: PRIOR FILING DATE: 2004-09-01
: NUMBER OF SEQ ID NOS: 25043
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 7343
:
: LENGTH: 2097
:
: TYPE: DNA
:
: ORGANISM: Zea mays
US-11-218-305-7343

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Query Match	13.2%	Score 486.2; DB 7	Length 2097;
Best Local Similarity	81.4%	Pred. No. 1.5e-83;	
Matches 500; Conservative	0;	Mismatches 126;	Indels 7; Gaps 2;

QY	239	GCTAGCTGAGTATCCAAAAGAAAGGCATACCAGTTAGTGTGTTGAATCACGACGA	298
Db	404	GCTAAGAGAGAGAGAGAGAGGTATACGTAAAGGACCGCGGCAACTAGTAACTAAC	463
QY	299	AGATGTCGTGCTCGCGGACGCGTGTGCTCCGCTGGCGTACAGGAGGACAACGTCGCGCTGG	358
Db	464	TGTCGTCGTCCGCGGAGCGACGATGCGCGTGGCGTACAG-----ACGTCGCGTCGT	517
QY	359	TGGCGGACTTGGCTAAACAAGGGGACACAGCGTGGCAGCTGTGGCGGCGACGCTGGTG	418
Db	518	CTCCCGATGTGCTGAACAAGGACGACAAACGCTGGCACTACGCGGCGACGCTGGTGG	577
QY	419	GAGTCGACAGGCTGCGCGGCTTGGTGTCGTATACGCGCGCGTGGTGAAGAAGTGGG	478
Db	578	GAGTCGACAGCTTCCCGAGTCTGGTGTGCTGTATACGCGCGCGTGGTGAAGAAGTGGG	637
QY	479	CGGTGAATCGGCGCTTCAATGGCGGCTTACAGCGCTTTCGCGCGGTGTGATCTTGGGTCA	538
Db	638	CGGTGAATCGGCGCTTCAATGGCGGCTTTCGCGCGGTGTGATCTTGGGTGGA	697
QY	539	CCTGGGCGTACACATGTGTTGGGAGAAAGCTCTCCGATCTGGGGGAAAGGCGCGG	598
Db	698	CCTGGGCGTACACATGTCTTTCGCGCGACAGGCTGTGCGCTGTGGGGCAAGGCGCGG	757
QY	599	CGGCGCTTGGACCAAGGCGCTCTCGTCGCGCGCGGCGCGCTGCGCGGACGAGTC--CACTAC	657
Db	758	CGGCGCTTGGACCAAGGCGCGCTCTCGTCGCGCGCGGCGCGCTTCCCGCACGCGCGCACAC	817
QY	658	CGCGCGGACGCGACGCGTGAACAGCGCGCGGCTGGAGCGCGTGAACCGCATGGCGAGCGGTG	717
Db	818	TTCGCGACGCGCGCTCTGGAGAACCCCGGCGCGGAGCGCGTGAACCGCATGGCGAGCGGTG	877
QY	718	GTTGATCTTCAAGTGGTGTTCGCGCGCATCAACCTCATCTGTGCGCGGCTCCCTCTC	777
Db	878	GTTGATCTTCAAGTGGTGTTCGCGCGCATCAACCTCATCTGTGCGCGGCTCCCTCTC	937
QY	778	GAGCGCATGAGCTTCTGCGCTGAGATATCTTTCGTCGCGGCTCTGGCTACACTTTCCTCAC	837
Db	938	GAGCGCATGAGCTTCTGCGCGCATGATGTCTTCGTCGCGGCTCTGGCTACACTTTCCTCAC	997
QY	838	ACCGTCGAGCGCTTCTCCCTCTGGGAGCGGAGCTCTCTTCACTGAGGAGCTCATCGAC	897
Db	998	ACCGTCGAGCGCTTCTCCCTCTGGGAGCGGAGCTCTCTTCACTGAGGAGCTCATCGAC	1057
QY	898	TACTCGGCGGCTACGTATCAACGTCCTGCGCGGACATGCGCGGCTTCAACGCGCGCTTAC	957
Db	1058	TACTCGGCGGCTACGTATCAACCTTCCGCTGGCTTCCGCGGATTCACGCGAGCTTAC	1117
QY	958	TGGGT 962	
Db	1118	TGGGT 1122	

QY 552 CATGTCGTCGCGGAGAAAGCTCTCCCATCTGGGGGAAAGCGCGCGCGCTGGACCA 611
DB 244 CATGGCGTTCCGCGCAACCGGCTCTCCGTTCTGGGGCAAGGCGGAGCGCTGAACGA 303
QY 612 GGGGCTCTCTGTCGCGCGCGCGCGCTGCGCGCAAGCTCACTACCGCGCGCAAGCGGAG 671
DB 304 GGACTCTCTGTCGCAACCGCGCGGTGTCTCCGCGCAAGCGGCACTACCGCGCAAGCGGAG 363
QY 672 CGTGAAGACGCGCGCGGTGGAAGCCGCTGTACCCGATGCGAGCGTGTATCTTCAAGTG 731
DB 364 GCTCAGACGCGCGCAACCGAGCCGTTCTACCGGAGGCGCGCTGTGTCTCTGTGAGTT 423
QY 732 CGTGTTCGCGCGCATACCCCTCATCTGTCGCGCGCTCTCTCTGCGCGCGATGAGCTT 791
DB 424 CGAGTTCCGCGCATACCCCTGTGTCTGTCGCGCGGTCTCTCTGCGCGCGATGAGCTT 483
QY 792 CCTGCGCTGATGATCTTGTGTCGCGCTGAGCTCACTTCTCTACACCGCTGCGCGCTT 851
DB 484 CAAGGCGTGGATGAGGAGTTCAACCGCTGAGCTCTCTCTCTACACCGCTGCGCGCTT 543
QY 852 CTCCTCTGCGCGCGCGCTTCTCTCTTCACTGCGCGCGCTCATGACTACTGCGCGGCTA 911
DB 544 CAGCTCTGCGCGCGCGCTTCTCTCTACGAGGCGCGCTCATGACTACTGCGCGGAGTA 603
QY 912 CGTCATCCACGTCCTCGCGCGCATGCGCGGCTTCAACCGCGCTTACTGAGT 962
DB 604 CGTCATCCACGTCCTCTCGCGCGCTGCGCGGCTTCAACCGCGCTACTGAGT 654

RESULT 10

US-10-449-902-26664

Sequence 26664, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

FILE REFERENCE: MOA-A02051-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 26664

LENGTH: 1719

TYPE: DNA

ORGANISM: Oryza sativa

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: AK102106

DATABASE ENTRY DATE: 2002-08-28

US-10-449-902-26664

Query Match 10.5%; Score 385.4; DB 6; Length 1719;
Best Local Similarity 74.5%; Pred. No. 2.8e-64;
Matches 485; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 312 GCGGACGCGTGGCGCTGGCGGATACGAGGGAACAGTGGGGTGGCGGCGGACTGGCT 371
DB 66 GCGGTGCGCGCGGACCGCGGCGGCGGATGCGGAGCTGCGCGGCTGCGCGGCTGGCT 125
QY 372 GAACAAGGGGGAACAAGCGTGGCGAGCTGGTGGCGGCAAGCTGTGTGGGCTGCAAGCGT 431
DB 126 GAACAAGGGGGAACAAGCGTGGCGAGCTGGTGGCGGCAAGCTGTGTGGGCTGCAAGCGT 185
QY 432 GCGGCGCTGT 491
DB 186 GCGTGGCGT 245

QY 492 GTTCATGCGGCTCTACGCGCTTCCGCGCGGTGTGATCTGCGGGTCACTGGGCGTACAA 551
DB 246 CTTATGCGGCTGTATGCGCTTACGCGCTTATGCTGTGTGTGTGTGTGTGTGTGTGTGT 305
QY 552 CATGTCGTCGCGGAGAAAGCTCTCCCATCTGGGGGAAAGCGCGCGCGCTGGACCA 611
DB 306 CATGGCGTTCCGCGCAACCGGCTCTCCGTTCTGGGGCAAGGCGGAGCGGCTGAACGA 365
QY 612 GGGGCTCTCTGTCGCGCGCGCGCGCTGCGCGCAAGCTCACTACCGCGCGCAAGCGGAG 671
DB 364 GCTCAGACGCGCGCAACCGAGCCGTTCTACCGGAGGCGCGCTGTGTCTCTGTGAGTT 423
QY 732 CGTGTTCGCGCGCATACCCCTCATCTGTCGCGCGCTCTCTCTGCGCGCGATGAGCTT 791
DB 424 CGAGTTCCGCGCATACCCCTGTGTCTGTCGCGCGGTCTCTCTGCGCGCGATGAGCTT 483
QY 792 CCTGCGCTGATGATCTTGTGTCGCGCTGAGCTCACTTCTCTACACCGCTGCGCGCTT 851
DB 484 CAAGGCGTGGATGAGGAGTTCAACCGCTGAGCTCTCTCTCTACACCGCTGCGCGCTT 543
QY 852 CTCCTCTGCGCGCGCGCTTCTCTCTTCACTGCGCGCGCTCATGACTACTGCGCGGCTA 911
DB 544 CAGCTCTGCGCGCGCGCTTCTCTCTACGAGGCGCGCTCATGACTACTGCGCGGAGTA 603
QY 912 CGTCATCCACGTCCTCGCGCGCATGCGCGGCTTCAACCGCGCTTACTGAGT 962
DB 604 CGTCATCCACGTCCTCTCGCGCGCTGCGCGGCTTCAACCGCGCTACTGAGT 654

RESULT 11

US-10-449-902-11363

Sequence 11363, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

FILE REFERENCE: MOA-A02051-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 11363

LENGTH: 1870

TYPE: DNA

ORGANISM: Oryza sativa

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: AK108711

DATABASE ENTRY DATE: 2002-08-28

US-10-449-902-11363

Query Match 10.1%; Score 372.6; DB 6; Length 1870;
Best Local Similarity 75.1%; Pred. No. 8.2e-62;
Matches 465; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 344 ACACGTCGCGCTGCGTGGCGGACTGCTGAACAAGGGGGAACAAGCGTGGGAGCTGTGG 403
DB 417 AGACCACTCCGTCATCGCGCAAGCTGTGTGAACAAGGGGGAACAAGCGTGGGAGATGAT 476
QY 404 CCGGCAAGCTGT 463
DB 477 CCGGCAAGCTGT 536

Qy	464	TGAAGAAGATGGGCGGTAACTCGGGGTTTCATGGCGCTCTACGGCTCGCCCGGCT	523
Db	537	TCTAGAAAGATGGGGCTATCAACTCGGGTTCAATGGCGCTGTATGGCTGTGCTGTCT	596
Qy	524	GGATCTGCTGGGTCACTCGGGCGTACACATGTGTTTGGGGAGAAAGTCTCTCCGACT	583
Db	597	GGATCTCTGGGTGTCTGGGCGATACACATGTGTTTGGGACCGCCTCTTGCCATTTCT	656
Qy	584	GGGGGAAGGCGGCGCGCTGGAGCAGAGGCTCTGTCGCGCGCGCGCTGCGCG	643
Db	657	GGGGTAAAGGCAAGGCGCAGCGCTCGGGCAGAGCTTCTGTGTGGCGCAGTTAGCTCACTG	716
Qy	644	CGACGGTTCACCTACCGGCGCCAGCGCAGCGCTGGAGACGGCGCGGTGAGCTCGTAC	703
Db	717	CTACCGCTATTGCTTACACACAAATGGGTGAGCTGAGGCGCCCATCTCAAGCGTGTAC	776
Qy	704	CGATGGGAGCGGTGTGTACTTTCAGTGCAGTGTTCGCGCGCATCACCTTACCTCCGTG	763
Db	777	CAGTCGCACCATGTGTGTACTTTCAGTGCAGTGTTCGAGAGCATACATCATCATCTCTG	836
Qy	764	CCGGCTCCCTCTCTGGCGCGCATGAGCTTCTCGGCTGGATGATCTTCGTCCCGCTTGCG	823
Db	837	CAGGCTACATGCTTGGGGCGATGAACATCAAGGCGTGGATGAGCTTTGTGCGGCTTGGA	896
Qy	824	TCACTCTTCTCTTAACCGTGGCGGCTTCTCCCTGTGGGGGGGGGAGTCTCTCTTTCAC	883
Db	897	TCACTCTTCTCTTAACCGTGTGGCGCTTCTGTGCTGTGGGGGGGGGAGTCTCTCTTTCAC	956
Qy	884	GGGGCGTATCGACTACGCGCGGCGTACATCATCAAGTCTCGCGCGGACATCGCGGCT	943
Db	957	GGGGTGTATGACTACTCTGTGGCTATGTATCATCATCTCTCTTGTGGACATCGAGGCC	1016
Qy	944	TCAACGCGGCTTACTGGGT 962	
Db	1017	TCACTGTCTCTACTGGGT 1035	

```

RESULT 12
US-10-713-648A-12
; Sequence 12, Application US/10713648A
; Publication No. US20060107344A1
; GENERAL INFORMATION:
; APPLICANT: POSCO
; APPLICANT: POSTECH
; APPLICANT: An, Gynheung
; APPLICANT: Ryu, Choong-Hwan
; APPLICANT: Han, Jong-Jin
; APPLICANT: Kang, Hong-Gyu
; APPLICANT: An, Kyungsok
; TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
; FILE OF INVENTION: MUTAGENESIS OF RICE
; FILE REFERENCE: 20010-04USA
; CURRENT APPLICATION NUMBER: US/10/713,648A
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/427,166
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) _ (96)
; OTHER INFORMATION: segment of the T-DNA insert in line 1C-109-35
US-10-713-648A-12

```

Query Match	8.5%	Score 312;	DB 6;	Length 401;
Best Local Similarity	97.0%;	Pred. No. 1.7e-50;		
Matches 318;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
Oy	2307	TGAGTTTTCTTGTGACGACGCAAGAAAAGCAGCTGAAAAATGAAATGGAATTTT	2366	

Db	74	TGNTTATTAAGTTGTCTAAGCAGCCAAAGAAAGCACACTGAAATAAATGAATATTT	133
QY	2367	TTTACAGCTCCCATTTCCGTGGGAGCACTTCGTCAAGCTATTTAGCGGGGAGGATGGA	2426
Db	134	TTAAGGCTCCCATTCCTGGGAGCACTTCGTCAAACTTAATTTAGCGGGGAGGATGGA	193
QY	2427	CTACAGACTCCATAGCAATTTGTGATGACATCAGGCACTGTCACTGTATCCGAAAGGA	2486
Db	194	CTACAGACTCCATAGCAATTTGTGATGACATCAGGCACTGTCACTGTATCCGAAAGGA	253
QY	2487	TCCGTGTCCTTATTATGACACACATGACAACCTTCAACCCCTTATCATTAATATTTGTT	2546
Db	254	TCCGTGTCCTTATTATGACACACATGACAACCTTCAACCCCTTATCATTAATATTTGTT	313
QY	2547	TTTAAATTTGGCGGATATATACAGATTTCAATPAGGCAATACATTAATTTTCTTTCC	2606
Db	314	TTTAAATTTGGCGGATATATACAGATTTCAATPAGGCAATACATTAATTTTCTTTCC	373
QY	2607	GTACACACACAGAACTCAATPAAATAAT	2634
Db	374	GTACACACACAGAACTCAATPAAATAAT	401

```

RESULT 13
US-11-216-545-4910
Sequence 4910, Application US/11216545
Publication No. US20060135758A1
GENERAL INFORMATION:
APPLICANT: MONSANTO Technology, LLC
APPLICANT: Mc Laird, Paul L
APPLICANT: Tao, Kunsheng
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53659)B
CURRENT APPLICATION NUMBER: US/11/216,545
CURRENT FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: US 60/606,062
PRIOR FILING DATE: 2004-08-31
NUMBER OF SEQ ID NOS: 8783
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4910
LENGTH: 1551
TYPE: DNA
ORGANISM: Glycine max
US-11-216-545-4910

```

Query Match	7.9% Beet Local Similarity	Score 289.6; 67.0% Matches 409;	DB 8; Pred. No. 6.1e-46; Conservative 0;	Mismatches 201; Indels 0; Gaps 0;
Qy	353	CGTCCGTGAGCGGATGTGGCTGTGAACAAGGAGGACAACGGGTGGCAGCTGGTGGCGGACGC	412	
Db	305	CGGCGGACACCGGATGGCTGTGAACAAGGTGACAACGGATGGCAGCTAAACGACGACCAACC	364	
Qy	413	TGATGGGAGCTGCAGAGCGGTGCGGAGCTTGTGTGCTGTACGCGCGGTGTGAAGAGA	472	
Db	365	TGCTGGGTCTTCAAAAGCATGCGGGGTCTGCGGATCTCTACGCGCAGCATAGTGAAGAAA	424	
Qy	473	AGTGGGCGGTGAATCTCGGCTTTCATGTGCGCTTACAGCTTCGCGCGGTGTGATCTTGCT	532	
Db	425	AATGGGACGTGAACTCAGCTTTCATGTGCTCTTACAGCTTTCGCGCGGTTCATATAGTT	484	
Qy	533	GGGTACACTGGGCGCTAACCATGTGCTGTGGGAGGAAGCTCTCCGATCTGGGAGGAGG	592	
Db	485	GGGTGCTTGTGTGTTCACGAATGGCTTTGGAGAGAACCTTTTCCTTCTGGGAGGAAGG	544	
Qy	593	CGCGGCGCGCGCTTGAACCAAGGAGCTCTCTGTGGCGCGCGCGCGCTGCACGCGTCC	652	
Db	545	GTGCTCCAGCAGCTATGGCGCAAGATGTTCTTACAGAAAGAGCCATAGTATTGAAACCATCC	604	
Qy	653	ACTACCGGCGCGACGCGCAGCGTGAAGACGGCGGGGTGTGAAGCCGCTTACCCGATGGGGA	712	

Db 605 ACCACTTGTGATATGATGCACTGTGATATCACTTCCTGAGGAACCTTTTACCTATGAGGCT 664
Qy 713 CGGTGCTGACTTCCAGTGCCTGTTGCGCGGCATCACTCTATCTCTGTCGGCGGTCCC 772
Db 665 CGCTGTGTATTTCCAAATTCACCTTTTGCTGCTATTACTCTATTTTGTGGCTGGCTCAG 724
Qy 773 TCCCTGGCGGCAGTGAAGCTTCTCGCTGATGATCTTGCTCCGCGCTGAGCTCACCTTCT 832
Db 725 TCCCTGGCGGCAGTGAAGCTTCTCGCTGATGATCTTGCTCCGCGCTGAGCTCACCTTCT 784
Qy 833 CCTACACGCTCGCGCTTCTCTCTCTGAGGCGCGCTTCTCTTCCACTGGGCGCTCA 892
Db 785 CCTACACAGTCCGGGCTTTAGCTTTGAGTGGGCTGTTGCTTCTCTCAACATGGGCGCTTA 844
Qy 893 TCGACTACTGCGCGCGCTCACTGATCACTGCTCTCCGCGGCATCGCGGCTTACCGCGC 952
Db 845 TTGACTATTTCTGGCGGCTATGTCATCCACCTTTCTTGAAATCGCTGGTTTAACTGCTG 904
Qy 953 CTTACTGGGT 962
Db 905 CTTACTGGGT 914

RESULT 14

US-10-953-349-17238
; Sequence 17238, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17238
; LENGTH: 805
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17238

Query Match 7.6%; Score 278; DB 6; Length 805;
Best Local Similarity 66.6%; Pred. No. 7, 5e-44;
Matches 398; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

Qy 365 ACTGCTGAACAAGGGGAGCAACGCTGGCAGCTGTGGCGGCGACGCTGTGGGGCTGC 424
Db 86 ACTGCTAAACAAGGGGAGCAACGCTGGCAGCTGTGGCGGCGACGCTGTGTAGGTCTCC 145
Qy 425 AGAGGCTGCGGGCTTGTGTGTCTGTACGGGCGGCTGTGAAGAAAGTGGCGGCTTA 484
Db 146 AAAGATGCGGGGTCTGTGTCTCTTACGCAAGTGTGAAGAAATGGCGGCTTA 205
Qy 485 ACTCGGCTTCAATGGGCTCTACGCTTTCGCGCGCTGTGATCTGCTGGTCACTTGG 544
Db 206 ACTCTGCAATTCATGGCGCTCTACGCTTTCGCGCGCTTCTAATATGCTGGTCTGTTT 265
Qy 545 GGTACCAATGTCTTGGGGAGAAAGCTCTTCCGATCTGGGGAGAAAGCGCGGCGGCGC 604
Db 266 GTCAACGATGGCTTGGGTGACAAACTGCTTCCCTTTCGGGGAGAGGCGCGCCCGAC 325
Qy 605 TGGACAGGCGCTCTCTGCTGCGCGCGCGCGCGCTGCGCGAGCGTCACTACCGCGCG 664
Db 326 TAGGCGAAGATTTTAAACAACCGCGCCAAAGTCCCGAAGACGCACTATTAACA 385
Qy 665 ACGGAGCGTGAAGACGCGCGGTGAGCGCGCTGTACCGGATGGCGAGGTGTGTACT 724
Db 386 ATGTATCGTGAAGACGCGAGCTTGGAAACGTTGTTTGCACGCGCTTCTTTGTATTT 445
Qy 725 TCAAGTGTGTGCGCGCATCACTCATCTGCTGCGCGGCTCTCTTCGCGCGCA 784

Db 446 TTCATTCACGTTTGGCGCTATCACGCTTATCTTGTGGCGGATCGGTGAGGAAGA 505
Qy 765 TGAAGTCTCGCGCTGAGTATCTTCGTCGCGCTGAGCTACCTTCTTCAACGCTG 844
Db 506 TGAACATCAAGGCTTGAAGTGTGTGCTTGTGCGCTTGTGCTGATTTTTCGACACTGTG 565
Qy 845 GCGCTTCTCCCTCTGGGAGCGCGGCTTCTCTTTCACGTGGGAGCTCAACGACTAGCG 904
Db 566 GGGCTTATAGCTTTGGGGTGGTGGCTTCTCTACATTTGGGGGCTTATGATTACTG 625
Qy 905 GCGCTACGTCATTCACGCTTTCGCGGAGATCGCGGCTTCAACCGCGCTTACTGGGT 962
Db 626 GTGATATGTTATTCATCTTCTCTGGAATGCTGTGCTTCACTGCTCTTACTGGGT 683

RESULT 15

US-10-953-349-10297
; Sequence 10297, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10297
; LENGTH: 1648
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10297

Query Match 5.8%; Score 214.8; DB 6; Length 1648;
Best Local Similarity 61.7%; Pred. No. 1, 3e-31;
Matches 379; Conservative 0; Mismatches 202; Indels 33; Gaps 1;

Qy 349 TCGGCGTGGGCGGAGCTGAGTGAACAAGGGGAGCAACGCTGGCAGCTGTGGCGGCG 408
Db 107 TTGCGGAGTTCCTGAAATGGCTCAACAAGGAGCAACGCTGGCAGCTTCAACGCGAGCG 166
Qy 409 ACGTGTGGGCTGCAAGCGTGGCGGCTTGTGTGTCTGTACGCGCGCGCTGTGAAG 468
Db 167 ACTGTGTGTGTCTACAGATGTCAGGTCTTGTATCTCTATGCTTCATGCTCAAG 226
Qy 469 AAGAGTGGCGGTAACTCGCGCTTCAATGCGCTTCAAGCTTTCGCGCGCTGTGATC 528
Db 227 AAGAAATGGCGTGAATTCAGCTTTATGCTCTTTAAGCTTTCGCGCGCTTCTTTC 286
Qy 529 TGTGTGTACCTGGGCGTAACAATGTCTTGGGAGAAAGCTCTCCGATCTGGGG 588
Db 287 TGTGTGTCTCTCTGTATCAAAATGCTTTTGAAGAAAGCTTTTGGCGGTGGG 346
Qy 589 AAGCGCGCGCGCTGAGCAAGGCGCTCTCTGTGCGCGCGCGCGCTGCGCGAGC 648
Db 347 AAAGTGTGTCACTTTCGACCAAGATACCTTAAGGAGCAAGAAAGTCTCC----- 399
Qy 649 GTTCACTACCGCGGAGGAGCGGCTGAGACGCGCGGTGTGAAGCGCTGTACCGCATG 708
Db 400 -----AAATGATTAATGTGGCGCGCGCTGATTTTCCGATG 433
Qy 709 GCGAGGTGTGTATCTTCAGTGTGCTTTCGCGCATCACCTCATCTGTCGCGGCG 768
Db 434 GCGAGGTGTGTATTTTCAATTCATTCGCGGAGTAACGACATCTTGTGGCGGAG 493
Qy 769 TCCCTCTCGCGCGATGAGCTTCTCTGCTGTGATCTTGTGCTCGCTGTGCTCAC 828
Db 494 TCTGTGTGGGAGGATGATATTAAGATGATGAGCTTTTGTGCAATGTGTGTATC 553
Qy 829 TTTCTCTACAGCTGTGGCGCTTCTCTCTGTGGGCGCGGCTTCTCTTCACTGGGCG 888
Db 554 TTTAGCTACAGTGTGAGCTTATGATATGGGAGGTGGGTTCTGTATCAGTGGGAG 613

QY 889 GTCATGACTACTGCGGCGCTAGTCATCAACGCTCCGCGGCAATCGCGGCTTCAAC 948
Db 614 GTTATTGATTATATCCGCGGCTATGTTATTCATCTCTCCGCGGTGTGCGGTTTCGTC 673
QY 949 GCGCTTACTGGGT 962
Db 674 GCTGCTTACTGGGT 687

Search completed: July 24, 2006, 02:05:07
Job time : 474 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:24:06 ; Search time 196 Seconds
(without alignments)
1117.381 Million cell updates/sec

Title: US-10-713-648a-63

Perfect score: 2534
Sequence: 1 MSSSATVVPPLAYQNTSASV.....GEMVDYTKRGSDAAVAVPVV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2534	100.0	479	8	ADP09672 Rice ammo
2	2216	87.5	470	6	AAO26538 Wheat hlg
3	2216	87.5	470	10	AEF16014 Trifolium
4	1891.5	74.6	509	8	ADY09035 plant ful
5	1860.5	73.4	486	6	AAO26537 Soybean h
6	1860.5	73.4	486	10	AEF16012 Glycine m
7	1715.5	67.7	497	6	AAO26536 Rice high
8	1715.5	67.7	497	10	AEF16010
9	1682.5	66.4	475	5	ABR92034
10	1357	53.6	325	7	ABM87942 Rice abio
11	1357	53.6	325	7	ABM90348 Rice abio
12	1352	53.4	440	7	ABM89810 Rice abio
13	717.5	28.3	455	7	ABO74999 Pseudomon
14	693.5	27.4	476	7	ABM87991 Rice abio
15	652	25.7	413	5	ABM84938
16	652	25.7	428	6	ABM70704
17	646	25.5	223	8	ADX89780
18	641	25.3	439	7	ABO66443 Klebsiell
19	640.5	25.3	488	6	ABP77916 N. gonorr
20	639	25.2	433	7	ADP05820 Bacterial
21	634.5	25.0	470	6	ADA34110 Actinoba
22	619.5	24.4	470	7	ABM87867 Rice abio
23	589.5	23.3	401	5	ABR49278 Listeria

24	589	23.2	428	6	ADA89710	Ada89710	Scaphyloc
25	589	23.2	428	6	ABM70882	Abm70882	Staphyloc
26	586.5	23.1	431	5	ABP65520	Abp65520	Bifidobac
27	583.5	23.0	191	8	ADX72255	Adx72255	Plant ful
28	582	23.0	437	5	ABP39062	Abp39062	Staphyloc
29	582	23.0	437	8	ADP07046	Adp07046	Staphyloc
30	565	22.3	438	4	AAQ93227	Aaq93227	C glutam
31	532	21.0	463	9	ABM96125	Abm96125	M. xanthu
32	522	20.6	479	8	ADR86206	Adr86206	Apergill
33	508	20.0	480	4	ADP98897	Adp98897	C. albica
34	476	18.8	452	4	AAE76708	Aae76708	Coryneb
35	476	18.8	452	4	AAQ93214	Aaq93214	C glutam
36	474.5	18.7	492	8	ADR78095	Adr78095	Yeast Str
37	422.5	16.7	924	4	ABG26085	Abg26085	Novel hum
38	342	13.5	651	2	ABR62422	AbR62422	Drosophil
39	338.5	13.4	501	2	AAE74676	Aae74676	Arabidops
40	338.5	13.4	501	3	AAQ40620	Aaq40620	Arabidops
41	338.5	13.4	510	3	AAQ36233	Aaq36233	Arabidops
42	335	13.2	361	7	ADH88022	Adh88022	Enterococ
43	335	13.2	514	8	ADN74427	Adn74427	Thale cre
44	322	12.7	431	7	ADM25447	Adm25447	Hyperther
45	320	12.6	446	3	AAQ40621	Aaq40621	Arabidops

ALIGNMENTS

RESULT 1	ADP09672	ADP09672 standard; protein; 479 AA.
ID	XX	ADP09672;
AC	XX	26-AUG-2004 (first entry)
DT	XX	Rice ammonium transporter protein without the T-DNA insert SegID 63.
DE	XX	
XX	XX	
KW	XX	rice; ammonium transporter; GUS; insertional mutagenesis;
KW	XX	beta-glucuronidase; biotic stress resistance; pesticide; herbicide;
KW	XX	plant; hygromycin phosphotransferase; HGH; T-DNA; transfer-DNA.
XX	XX	
OS	XX	Oryza sativa.
PN	XX	WO2004046357-A1.
XX	XX	
PD	XX	03-JUN-2004.
XX	XX	
PR	XX	14-NOV-2003; 2003WO-KR002461.
XX	XX	
PF	XX	15-NOV-2002; 2002US-0427166P.
XX	XX	
PA	XX	(POSC-) POSCO.
XX	XX	(POST-) POSTECH FOUNO.
XX	XX	
PI	XX	An G, Ryu C, Han J, Kang H, An K;
XX	XX	
DR	XX	WPI; 2004-449751/42.
XX	XX	N-PSDB; ADP09638, ADP09655.
XX	XX	
PT	XX	New organ preferential nucleic acids and polypeptides, useful in
XX	XX	producing rice plants with desired characteristics and which are
PT	XX	resistant to herbicide, plant pathogen, fungi, bacteria, virus, insect,
XX	XX	nematode, and stress.
PS	XX	Claim 15; SEQ ID NO 63; 296pp; English.
XX	XX	
CC	XX	This invention relates to a novel method of identifying nucleic acid
CC	XX	molecules, or fragments thereof, that are expressed in an organ
CC	XX	preferential manner in rice. Specifically, it refers to producing rice
CC	XX	cell lines that carry tagged genes modified by T-DNA/GUS based
CC	XX	insertional mutagenesis, where the GUS portion of the insert is the
CC	XX	promoterless beta-glucuronidase reporter gene that can only be expressed
CC	XX	when it is inserted into an active gene. The present invention describes

CC generating transformed rice lines containing transfer-DNA (T-DNA)
CC insertions that also carry a gene encoding the selectable marker
CC hygromycin phosphotransferase (Hph). Accordingly, this method can be used
CC to produce rice plants with desirable characteristics including increased
CC grain yield and nutritional content, resistance to biotic stresses,
CC pesticides, herbicides or insects, altered morphology or improved
CC characteristics referring to shape, taste or cooking quality of the
CC grain. This polypeptide sequence represents a rice protein encoded by a
CC gene that will be T-DNA/GUS tagged for expression analyses, given in an
CC exemplification of the invention.

CC Sequence 479 AA;

Query Match 100.0%; Score 2534; DB 8; Length 479;

Best Local Similarity 100.0%; Pred. No. 8.8e-235; Mismatches 0; Indels 0; Gaps 0;

Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSATVPLAYQNTSASVADMLKGNAMQLVAATLVGLQSVPLVLYGGVKKKMA 60
DB 1 MSSATVPLAYQNTSASVADMLKGNAMQLVAATLVGLQSVPLVLYGGVKKKMA 60
QY 61 VNSAFMALYAFPAVMI CWVTMAVYNNMSPGKLLPIWGKAPALDQGLVGRALPATVHYR 120
DB 61 VNSAFMALYAFPAVMI CWVTMAVYNNMSPGKLLPIWGKAPALDQGLVGRALPATVHYR 120
QY 121 ADGSETAVERPLYPMATVYVFCVFAATLTLVAGSLIGRMSFLAMMIFVPLMTFSYT 180
DB 121 ADGSETAVERPLYPMATVYVFCVFAATLTLVAGSLIGRMSFLAMMIFVPLMTFSYT 180
QY 181 VQAFSLMGSGFLPHNGVIDYCGGVYIHVSAGIAGFTAAVWGPRAQKORERPPNNILFT 240
DB 181 VQAFSLMGSGFLPHNGVIDYCGGVYIHVSAGIAGFTAAVWGPRAQKORERPPNNILFT 240
QY 241 LTGAGLLMGMAGFNGGCPYAAANSVASMAVLTNTICTAMSLIWTCLDVIFFKKSQVGA 300
DB 241 LTGAGLLMGMAGFNGGCPYAAANSVASMAVLTNTICTAMSLIWTCLDVIFFKKSQVGA 300
QY 301 VQGMITGLVCTIPRAGVVOGMAALVMGVLAGSIPWYTMMLHKRSKILQVDDTLGVPH 360
DB 301 VQGMITGLVCTIPRAGVVOGMAALVMGVLAGSIPWYTMMLHKRSKILQVDDTLGVPH 360
QY 361 HGVAGLLGLLTLGLFAEPTLCNLFLPVADSRGAFYGAAGAOFKQIAGLFFVAMNVV 420
DB 361 HGVAGLLGLLTLGLFAEPTLCNLFLPVADSRGAFYGAAGAOFKQIAGLFFVAMNVV 420
QY 421 TSLICLAIVLPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTKHGSDAAVAPVV 479
DB 421 TSLICLAIVLPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTKHGSDAAVAPVV 479

RESULT 2

AAO26538 ID AAO26538 standard; protein; 470 AA.

AAO26538; AC

18-FEB-2003 (first entry)

Wheat high affinity ammonium transporter protein #2.

Herbicide; ammonium transporter protein; herbicide; transgenic plant;

Wheat.

Triticum aestivum.

US2002142390-A1.

03-OCT-2002.

28-DEC-2001; 2001US-00033109.

28-AUG-1998; 98US-0084248P.

27-AUG-1999; 99US-00384625.

XX (ALLEN) ALLEN S M.
PA (RAFA) RAFALSKI J A.
XX Allen SM, Rafalski JA;
XX WPI; 2003-102520/09.
DR N-PsDB; AAL53990.
XX Novel ammonium transporter polypeptide useful for identifying enzymatic
PT inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
PT transporter polypeptides.

PS Claim 14; Page 24-25; 27pp; English.

CC The invention relates to a novel ammonium transporter protein comprising
CC 90% homology based on the Clustal method compared to: a corn ammonium
CC transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
CC transporter polypeptide of 500 or 486 amino acids; a wheat ammonium
CC transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
CC transporter 497 amino acids fully defined in the specification. The
CC isolated polynucleotide is useful for selecting an isolated
CC polynucleotide that affects the level of expression of the ammonium
CC transporter polypeptide in a plant cell. The ammonium transporter protein
CC is useful for preparing antibodies which are useful for detecting the
CC transporter protein in situ in cells or in vitro in cell extracts, and as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that are useful as herbicides. The isolated polynucleotide is also useful
CC for creating transgenic plants in which the polynucleotide is present at
CC higher or lower levels than normal, and for designing and producing
CC primer pairs which are useful in amplification or primer extension
CC reactions. This sequence represents the wheat high affinity ammonium
CC transporter protein of the invention

XX Sequence 470 AA;

Query Match 87.5%; Score 2216; DB 6; Length 470;

Best Local Similarity 86.0%; Pred. No. 3.6e-204; Mismatches 34; Indels 2; Gaps 1;

Matches 404; Conservative 30; Mismatches 34; Indels 2; Gaps 1;

QY 8 VPLAYQNTSASVADMLKGNAMQLVAATLVGLQSVPLVLYGGVKKKMAVNSAFMA 67
DB 3 VPAVQNTSAAVADMLKGNAMQLTASTLVGLMSVGMVLYGGVKKKMAVASAFMA 62
QY 68 LYAPFAVMI CWVTMAVYNNMSPGKLLPIWGKAPALDQGLVGRALPATVHYRADSGVET 127
DB 63 LYAPFAVMI CWVTMAVYNNMSPGKLLPIWGKAPALDQGLVGRALPATVHYRADSGVET 122
QY 128 AAVEPLYPMATVYVFCVFAATLTLVAGSLIGRMSFLAMMIFVPLMTFSYTGAFFSLW 187
DB 123 AAVEPLYPMATVYVFCVFAATLTLVAGSLIGRMSFLAMMIFVPLMTFSYTGAFFSLW 182
QY 188 GGGFLFWHGVIDYCGGVYIHVSAGIAGFTAAVWGPRAQKORERPPNNILFTLTGAGLL 247
DB 183 GGGFLFWHGVIDYCGGVYIHVSAGIAGFTAAVWGPRAQKORERPPNNILFTLTGAGLL 242
QY 248 WMGAGFNGGCPYAAANSVASMAVLTNTICTAMSLIWTCLDVIFFKKSQVGAOGMTTG 307
DB 243 WMGAGFNGGCPYAAANSVASMAVLTNTICTAMSLIWTCLDVIFFKKSQVGAOGMTTG 302
QY 308 LVCITPRAGVVOGMAALVMGVLAGSIPWYTMMLHKRSKILQVDDTLGVHTHGVAGLL 367
DB 303 LVCITPRAGVVOGMAALVMGVLAGSIPWYTMMLHKRSKILQVDDTLGVHTHGVAGLL 362
QY 368 GGLTLGLFAEPTLCNLFLPVADSRGAFYGAAGAOFKQIAGLFFVAMNVVTSLICLA 427
DB 363 GGLTLGLFAEPTLCNLFLPVADSRGAFYGAAGAOFKQIAGLFFVAMNVVTSLICIV 422
QY 428 INLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTKHGSDAAVAPV 477
DB 423 IRLVPLRMSSEKLAIGDDAVHGEBAVALMGDEMYDVTKHGSDAAVAPV 470

CC invention.
XX Sequence 509 AA;

Query Match 74.6%; Score 1891.5; DB 8; Length 509;
Best Local Similarity 72.9%; Pred. No. 76-173;
Matches 341; Conservative 57; Mismatches 61; Indels 9; Gaps 4;

QY 11 AVOGNTSADVADMLKNDAMQVLAATLVGLQSVGLVYLGGVYKKKVAVSAPMALYA 70
DB 38 AVO--SSSAPMLNKGDNAMQMTSKVLVGLQSMFGLVLYGSIVYKKKVAVSAPMALYA 95
QY 71 FAAVVICWTTAAVYNNSSFGKELPIWGKAPALDQGLVGRALPAT-VHYRADGSVETAA 129
DB 96 FAAVVICWTTAAVYNNSSFGKELPIWGKAPALDQGLVGRALPAT-VHYRADGSVETAA 154
QY 130 VEPYLPMAVTVFQCVFAATITLILVAGSLGMSFLAMMI FVPLMLTFSYTYGAFLMG 189
DB 155 LHPFPAATIMVYFQCVFASITVITILAGSLGMDIKAMWAFVPLMLTFSYTYGAFLMG 214
QY 190 GFLPHMGVIDYCGVYVHVSAGIAGFTAAVYWGPRAPKORERPPNNILFTLTGAGLLM 249
DB 215 GFLPHMGVIDYCGVYVHVSAGIAGFTAAVYWGPRAPKORERPPNNILFTLTGAGLLM 274
QY 250 GWAGFNCGGPRYAANSVASMALVNTNICTAMSLIWTCLDVIFFKKPSVAVQGMITGLV 309
DB 275 GWTFNGGDPYSANIDSSMAVLTNTHICATSLMLMTLDVFFPKPSVIGAVQGMITGLV 334
QY 310 CITPAAGVVGMAALVVGVLASIPYTTMILHKSKILQVDDTLGVFHTGAVAGLLG 369
DB 335 CITPAAGVVGMAALVVGVLASIPYTTMILHKSKILQVDDTLGVFHTGAVAGLLG 394
QY 370 LITGLFAEPTLCNLFPLVADSRGAFYGGAGAGOFKQIAGLFVVAANVVTSLICLAI 429
DB 395 ATTGFAEPTLCNLFPLVADSRGAFYGGAGAGOFKQIAGLFVVAANVVTSLICLAI 454
QY 430 LILVPLRMPDDKLEVGDDAVHGEAVALMGDGEYDVT-----KHGSDA 472
DB 455 LILVPLRMPDDKLEVGDDAVHGEAVALMGDGEYDVT-----KHGSDA 502

RESULT 5
AA026537
ID AA026537 standard; protein; 486 AA.

AC AA026537;

DT 18-FEB-2003 (first entry).

DE Soybean high affinity ammonium transporter protein #2.

KM Herbicide; ammonium transporter protein; herbicide; transgenic plant;
XX soybean.

OS Glycine max.

PN US2002142390-A1.

PD 03-OCT-2002.

XX 28-DEC-2001; 2001US-00031109.

XX 28-AUG-1998; 98US-0098248P.

PR 27-AUG-1999; 99US-00384625.

PA (ALIE/) ALLEN S M.

PA (RAFA/) RAFALSKI J A.

PI Allen SM, Rafalski JA;

DR WPI, 2003-102520/09.

DR N-PSDB; AAL53989.

XX

PT Novel ammonium transporter polypeptide useful for identifying enzymatic
PT inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
PT transporter polypeptides.

PS Claim 14; Page 22-23; 27pp; English.

XX The invention relates to a novel ammonium transporter protein comprising
CC 90% homology based on the Clustal method compared to: a corn ammonium
CC transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
CC transporter polypeptide of 500 or 466 amino acids; a wheat ammonium
CC transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
CC transporter 497 amino acids fully defined in the specification. The
CC isolated polynucleotide is useful for selecting an isolated
CC polynucleotide that affects the level of expression of the ammonium
CC transporter polypeptide in a plant cell. The ammonium transporter protein
CC is useful for preparing antibodies which are useful for detecting the
CC transporter protein in situ in cells or in vitro in cell extracts, and as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that are useful as herbicides. The isolated polynucleotide is also useful
CC for creating transgenic plants in which the polynucleotide is present at
CC higher or lower levels than normal, and for designing and producing
CC primer pairs which are useful in amplification or primer extension
CC reactions. This sequence represents the soybean high affinity ammonium
CC transporter protein of the invention

CC Sequence 486 AA;

Query Match 73.4%; Score 1860.5; DB 6; Length 486;
Best Local Similarity 71.9%; Pred. No. 6.3e-170;
Matches 341; Conservative 51; Mismatches 77; Indels 5; Gaps 2;

QY 9 PLAVOAGNTSADVADMLKNDAMQVLAATLVGLQSVGLVYLGGVYKKKVAVSAPMAL 68
DB 4 PLAVOAGNTSADVADMLKNDAMQVLAATLVGLQSVGLVYLGGVYKKKVAVSAPMAL 62

QY 69 YAFPAVVICWTTAAVYNNSSFGKELPIWGKAPALDQGLVGRALPAT-VHYRADGSVETAA 128
DB 63 YAFPAVVICWTTAAVYNNSSFGKELPIWGKAPALDQGLVGRALPAT-VHYRADGSVETAA 122

QY 129 AVEPLYPMAVTVFQCVFAATITLILVAGSLGMSFLAMMI FVPLMLTFSYTYGAFLMG 188
DB 123 AVEPLYPMAVTVFQCVFAATITLILVAGSLGMSFLAMMI FVPLMLTFSYTYGAFLMG 182

QY 189 GGLFPHMGVIDYCGVYVHVSAGIAGFTAAVYWGPRAPKORERPPNNILFTLTGAGLLM 248
DB 183 GGLFPHMGVIDYCGVYVHVSAGIAGFTAAVYWGPRAPKORERPPNNILFTLTGAGLLM 242

QY 249 MGWAGFNCGGPRYAANSVASMALVNTNICTAMSLIWTCLDVIFFKKPSVAVQGMITGL 308
DB 243 MGWAGFNCGGPRYAANSVASMALVNTNICTAMSLIWTCLDVIFFKKPSVAVQGMITGL 302

QY 309 CITPAAGVVGMAALVVGVLASIPYTTMILHKSKILQVDDTLGVFHTGAVAGLLG 368
DB 303 CITPAAGVVGMAALVVGVLASIPYTTMILHKSKILQVDDTLGVFHTGAVAGLLG 362

QY 369 GILTGLFAEPTLCNLFPLVADSRGAFYGGAGAGOFKQIAGLFVVAANVVTSLICLAI 428
DB 363 GILTGLFAEPTLCNLFPLVADSRGAFYGGAGAGOFKQIAGLFVVAANVVTSLICLAI 422

QY 429 NILVPLRMPDDKLEVGDDAVHGEAVALMGDGEYDVT-----DAAVAPV 478
DB 423 NILVPLRMPDDKLEVGDDAVHGEAVALMGDGEYDVT-----DAAVAPV 476

RESULT 6
AEF16012
ID AEF16012 standard; protein; 486 AA.

AC AEF16012;

DT 09-MAR-2006 (first entry)

DE Glycine max ammonium transporter protein Segid12.

XX ammonium transfer; transgenic plant; nitrogen; cellular transport.
KW Glycine max.
OS US2006010512-A1.
XX 12-JAN-2006.
PD 15-DEC-2004; 2004US-00012668.
PF 28-DEC-2001; 2001US-00033109.
XX (ALIE/) ALLEN S M.
XX (RAFA/) RAFALSKI J A.
XX Allen SM, Rafaleki JA;
PI MPI, 2006-088761/09.
DR N-PSDB; AEF16011.
XX New isolated polynucleotide encoding a polypeptide having ammonium
PT transfer activity, useful for producing transgenic plants with increased
XX nitrogen content.
XX Example 4; SEQ ID NO 12; 29pp; English.
XX This invention relates to a novel isolated polynucleotide encoding a
CC polypeptide having ammonium transfer activity. The polynucleotides are
CC useful for producing transgenic plants with increased nitrogen content.
CC The present sequence is an ammonium transporter protein which is encoded
CC by a nucleotide sequence homologous to the sequence of the invention.
XX
SQ Sequence 486 AA;

Query Match 73.4%; Score 1860.5; DB 10; Length 486;

Best Local Similarity 71.9%; Pred. No. 6.3e-170; Indels 5; Gaps 2;
Matches 341; Conservative 51; Mismatches 77;

QY 9 PLAYOGNTSASVADWLNKGDNAWQVAATLVGLQSVGLVLYGGVKKKMAVNSAFMAL 68
DB 4 PLAYQEHLEPA-PENLNKGDNAWQVAATLVGLQSVGLVLYGGVKKKMAVNSAFMAL 62
QY 69 YAPAAVWICWTVWYVMSFGKELPIWGRAPALDQGLIVGRAALPATVHYRADSGVEYA 128
DB 63 YAPAAVWICWTVWYVMSFGKELPIWGRAPALDQGLIVGRAALPATVHYRADSGVEYA 122
QY 129 AVEPLYPMAVTVVFOCVFAATLILVAGSLGRMSFLAMMIFVPLMTFTSYTGAFSLMG 188
DB 123 PEEPPYPMASLYVFPQTFPAITLILLAGSVLGRMNIKAMMAFVPLMLFTSYTGAFSLMG 182
QY 189 GGFLEFMGVYIDYCGGVIVHSAGIAGFTAAVYVGPRAOKDRERFPNNILFTLTGAGLIM 248
DB 183 GGFLEFMGVYIDYCGGVIVHSAGIAGFTAAVYVGPRAOKDRERFPNNILFTLTGAGLIM 242
QY 249 MGNAGFNGGAPYAANSVASMAVANTINI CTAMSLIVTCLDIVFEKKPSVAGVQGMITGL 308
DB 243 MGNAGFNGGAPYAANSVASMAVANTINI CTAMSLIVTCLDIVFEKKPSVAGVQGMITGL 302
QY 309 VCTTPAAGVYQGAALVYMGVLAGSIWYTMILHRSKSLQKRDPTLGVFHTGAVGLIG 368
DB 303 VCTTPAAGVYQGAALVYMGVLAGSIWYTMILHRSKSLQKRDPTLGVFHTGAVGLIG 362
QY 369 GILTTGFAEPTLCNLFPLPVADSRGAFYGGAGAQFGKQIAGLFLVAVAMVVTSLICLAI 428
DB 363 GILTTGFAEPTLCNLFPLPVADSRGAFYGGAGAQFGKQIAGLFLVAVAMVVTSLICLAI 422
QY 429 NILVPLRMPDDKLEVGDDAVHGEAAVALMGDGEYDVTYKGS---DAVAAPVY 478
DB 423 NILVPLRMPDDKLEVGDDAVHGEAAVALMGDGEYDVTYKGS---DAVAAPVY 476

RESULT 7

AA026536
ID AA026536 standard; protein; 497 AA.
XX
XX AA026536;
AC 18-FEB-2003 (first entry)
DT Rice high affinity ammonium transporter protein.
XX
XX Herbicide; ammonium transporter protein; herbicide; transgenic plant;
KW rice.
XX
XX Oryza sativa.
OS
XX US2002142390-A1.
XX 03-OCT-2002.
PD 28-DEC-2001; 2001US-00033109.
PF 28-AUG-1998; 98US-0098248P.
PR 27-AUG-1999; 99US-00384625.
XX (ALIE/) ALLEN S M.
XX (RAFA/) RAFALSKI J A.
XX Allen SM, Rafaleki JA;
PI MPI, 2003-102520/09.
DR N-PSDB; AAL53988.
XX Novel ammonium transporter polypeptide useful for identifying enzymatic
PT inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
PT transporter polypeptides.
XX
XX Claim 14; Page 20-21; 27pp; English.
PS
XX The invention relates to a novel ammonium transporter protein comprising
CC 90% homology based on the Clustal method compared to: a corn ammonium
CC transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
CC transporter polypeptide of 500 or 486 amino acids; a wheat ammonium
CC transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
CC transporter 497 amino acids fully defined in the specification. The
CC isolated polynucleotide is useful for selecting an isolated
CC polynucleotide that affects the level of expression of the ammonium
CC transporter polypeptide in a plant cell. The ammonium transporter protein
CC is useful for preparing antibodies which are useful for detecting the
CC transporter protein in situ in cells or in vitro in cell extracts, and as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that are useful as herbicides. The isolated polynucleotide is present at
CC higher or lower levels than normal, and for designing and producing
CC primer pairs which are useful in amplification or primer extension
CC reactions. This sequence represents the rice high affinity ammonium
CC transporter protein of the invention
XX
SQ Sequence 497 AA;

Query Match 67.7%; Score 1715.5; DB 6; Length 497;

Best Local Similarity 69.3%; Pred. No. 6e-156;
Matches 312; Conservative 54; Mismatches 83; Indels 1; Gaps 1;

QY 19 SVADWLNKGDNAWQVAATLVGLQSVGLVLYGGVKKKMAVNSAFMALYAPAAVWICW 78
DB 16 AVBEMWNTGDNQWQJLAATFVGLQSVGLVLYGGVKKKMAVNSAFMALYAPAAVWICW 75
QY 79 YMAVYMSFGKELPIWGRAPALDQGLIVGRAALPATVHYRADSGVEYAAVEPTLPMAT 138
DB 76 YMAVYMSFGKELPIWGRAPALDQGLIVGRAALPATVHYRADSGVEYAAVEPTLPMAT 135
QY 139 VVYFQCVFAATLILVAGSLGRMSFLAMMIFVPLMTFTSYTGAFSLMGGFLPFHMGVI 198
DB 136 VVYFQCVFAATLILVAGSLGRMSFLAMMIFVPLMTFTSYTGAFSLMGGFLPFHMGVI 195

QY DYCGGYVHVHVSAGIAGFTAAVWVSPRAOKRERPPNNILFTLTGAGLMMGMAGFNGGG 258
DB DSGGIVHLHSGIGFTDAVWVSPRLKSDRERSBNLIMLAGGLMMAGFNGGA 255
QY PYAANSVASMALNTNICTAMSLIWTCLVDYIFPKKPSVGAVOGMTGLVCITPAAGV 318
DB PYAPRITASIVLNTNVSAAASLTLWTCLVDYIFPKKPSVIGAVQGMGTGLVCITPAAGV 315
QY OGMAALVWGVLAGSIPIWYTMILHKRSKILQKVDTLGFTHTHVAAGLLGGLTGLFPAEP 378
DB HTMAAILMGICGGSIPWFSMILHKRSALLQKVDTLAVFHTHVAAGLLGGLTGLFPAEP 375
QY TLGNLFPLPADSRGAFYFGAGAGFGKOIAGGLFVAVMNVVTSILCLAINLVLPLRMPD 438
DB DLTAVHTHIPGARGAFYFG-GIAOVGKQIAGALFVAVMNVVATTVILGVLVPLRMPD 434
QY DKLEVGDDAVHGEBAVYALMGDEMYDVTKH 468
DB EQLKIGDDAHGEBAVYALMGDERFDVTRH 464

RESULT 8

AEF16010
ID AEF16010 standard; protein; 497 AA.

AC AEF16010;

DT 09-MAR-2006 (first entry)

DE Oryza sativa ammonium transporter protein Seqid10.

KM ammonium transfer; transgenic plant; nitrogen; cellular transport.

XX Oryza sativa.

PN US2006010512-A1.

PD 12-JAN-2006.

PF 15-DEC-2004; 2004US-00012668.

PR 28-DEC-2001; 2001US-00033109.

PA (AILE/) ALLEN S M.

PI (RAFA/) RAFALSKI J A.

PI Alien SM, Rafalski JA;

DR WPI: 2006-088761/09.

DR N-PSDB; AEF16009.

PT New isolated polynucleotide encoding a polypeptide having ammonium transfer activity; useful for producing transgenic plants with increased nitrogen content.

PS Example 4; SEQ ID NO 10; 29pp; English.

CC This invention relates to a novel isolated polynucleotide encoding a polypeptide having ammonium transfer activity. The polynucleotides are useful for producing transgenic plants with increased nitrogen content.

CC The present sequence is an ammonium transporter protein which is encoded by a nucleotide sequence homologous to the sequence of the invention.

XX Sequence 497 AA;

SQ

Query Match 67.7%; Score 1715.5; DB 10; Length 497;

Best Local Similarity 69.3%; Pred. No. 6e-156; Mismatches 83; Indels 1; Gaps 1;

Matches 312; Conservative 54; Mismatches 83; Indels 1; Gaps 1;

QY 19 SVADNINKDNAMQVLAATLVGLQSVFGLVLYGVVKKKKAIVNSAFMALVFAAVWICW 78
DB 16 AVPEWMLNTGDNQMQLAAATFVGLQSWPGLVLYGVISVKKKKAIVNSAFMALVYASTLIW 75

QY VTMAVNSFGEKLLPIWGKARPALDOGLVGRALPATVHYRADGSYETAABEPLYMAT 138
DB VLVGFRMAFGRLLPFMCKAGALLTEGFLVARASVPATAHGKGALESPTTEFFYPBAS 135
QY 139 VVYPCVFAATITLLVAGSLGRMSFLAMMI FVBLMLTFSTYVGAFSIMGGFLPHWCVI 198
DB MVLQFELAAITLVLLAGSLIGRMNIRKAMNAFTPLMLFSYTVCAFSIMGGFLYQWCVI 195
QY 199 DYCGGYVHVHVSAGIAGFTAAVWVSPRAOKRERPPNNILFTLTGAGLMMGMAGFNGGG 258
DB DSGGIVHLHSGIGFTAAVWVSPRLKSDRERSBNLIMLAGGLMMAGFNGGA 255
QY PYAANSVASMALNTNICTAMSLIWTCLVDYIFPKKPSVGAVOGMTGLVCITPAAGV 318
DB PYAPRITASIVLNTNVSAAASLTLWTCLVDYIFPKKPSVIGAVQGMGTGLVCITPAAGV 315
QY OGMAALVWGVLAGSIPIWYTMILHKRSKILQKVDTLGFTHTHVAAGLLGGLTGLFPAEP 378
DB HTMAAILMGICGGSIPWFSMILHKRSALLQKVDTLAVFHTHVAAGLLGGLTGLFPAEP 375
QY TLGNLFPLPADSRGAFYFGAGAGFGKOIAGGLFVAVMNVVTSILCLAINLVLPLRMPD 438
DB DLTAVHTHIPGARGAFYFG-GIAOVGKQIAGALFVAVMNVVATTVILGVLVPLRMPD 434
QY DKLEVGDDAVHGEBAVYALMGDEMYDVTKH 468
DB EQLKIGDDAHGEBAVYALMGDERFDVTRH 464

RESULT 9

ABB92034
ID ABB92034 standard; protein; 475 AA.

AC ABB92034;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 1245.

KM Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN WO200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EP009892.

PR 28-AUG-2001; 2001WO-EP009892.

PA (FARB) BAYER AG.

PI Tietjen K, Weidler M;

DR WPI: 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.

CC The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected.

CC The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as

PS Claim 5; SEQ ID NO 1245; 261pp + Sequence Listing; English.

CC The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected.

CC The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as

CC The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected.

CC The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as

CC herbicides
 XX Sequence 475 AA;
 SQ Query Match 66.4%; Score 1682.5; DB 5; Length 475;
 Best Local Similarity 66.8%; Pred. No. 8,4e-153;
 Matches 300; Conservative 61; Mismatches 77; Indels 11; Gaps 1;

QY 20 VADMLNKGNDAWOLVAATLVGLQSPGLVYL YGGVVKKKKNAVNSAFMALYAFPAWICWV 79
 DB 12 VPEMLNKGNDAWOLVAATLVGLQSPGLVYL YSIVKKKNAVNSAFMALYAFPAWICWV 71
 QY 80 TMAVNSFGEKLPINGKARPALDOGLVGRALPATVHVRADGSVETAVERELYPMATV 139
 DB 72 LICYKNAFGEELLPENKGGPAPDQGLYKQQAIP-----NSNVAAPFPFPAATL 120
 QY 140 VYFCQFAATTLTLVAGSLGRMSFLAMWIFVPLMLFTSYTGAFSLMGGFLFHWGVID 199
 DB 121 VYFQFPAATTLTLVAGSVLGRNIRKAMAFVPLMLFSTTVGAYSTMGSGFLYQMCVID 180
 QY 200 YCGGYVIVHAGIAGFTAAVVGPPRAQKDRERFPNNILFTLTGAGLLMAGNPGGCP 259
 DB 181 YSGGYVIVHSSGVAAGFVAATVWGPPEKADREPRPNNVILMLAGAGLLMAGSGFNGCAP 240
 QY 260 YAANSVASMAYLNTNICTMSLIVWTCLDVIFPKKSVGAVAGQMTGLVCITPAAGVQ 319
 DB 241 YAANLTSSIAVLNTNISAATSLVWTTLDVIFPKKSVIGALQSMVYGLAGVTPGAGLIQ 300
 QY 320 GMAALVAGVLASIPWYTMMLHKRSKILQVVDTLGVFTHGVAGLLGLTGLFAEPT 379
 DB 301 TMAAIIIGVSGTRAPNASMMIHKKSALLQKDDTLAVFTHAVAGLLGSGIMTGLFAHPD 360
 QY 380 LCNLFLPVADSRGAFYGGAGCAQFGKQIAGGLFVAVANNVVTSLICLAINLVLPLMPDD 439
 DB 361 LCVLVLPLPATRGAFYGGNGKQLKQLAGAFLAVNNVSTIILLAIHVFIPLMAEE 420
 QY 440 KLEVGDDAVHGERAVYALMGDEMYDVYTKH 468
 DB 421 ELGIGDDAAHGEBAVYALMGDEKFDATRH 449

RESULT 10
 ABM87942
 ID ABM87942 standard; protein; 325 AA.
 AC ABM87942;
 XX 02-JUN-2005 (first entry)
 DT Rice abiotic stress responsive polypeptide SEQ ID NO:6188.
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:6188.
 KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX Oryza sativa.
 OS
 XX
 XX WO2003008540-A2.
 PN 30-JAN-2003.
 PD 21-JUN-2002; 2002WO-US019668.
 PF 22-JUN-2001; 2001US-0300112P.
 PR 24-AUG-2001; 2001US-0314662P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 21-NOV-2001; 2001US-0332132P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
 PI Moughamer T, Provart N, Rieke D, Zhu T;
 XX WPI; 2003-248011/24.

PT New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 XX
 XX Claim 1; SEQ ID NO 6188; 89pp; English.
 XX
 CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention

XX
 SQ Sequence 325 AA;
 Query Match 53.6%; Score 1357; DB 7; Length 325;
 Best Local Similarity 76.5%; Pred. No. 1.1e-121;
 Matches 248; Conservative 30; Mismatches 40; Indels 6; Gaps 2;

QY 1 MSSSATVPLAYQGNSTASVADMLNKGNDAWOLVAATLVGLQSPGLVYL YGGVVKKKNA 60
 DB 1 MSGDAFNMSVAVQPSGMA-VPEWLNKGNDAWOMISATLVGMSVPLVILYGSIVKKKNA 59
 QY 61 VNSAFMALYAFPAWICWYTMVAVNSFGEKLPINGKARPALDOGLVGRALPATVH- 119
 DB 60 VNSAFMALYAFPAWICWYTMVAVNSFGEKLPINGKARPALDOGLVGRALPATVH- 119
 QY 120 ---RADGSVETPAVEPLYPMATVYVFCQVFAITLTLVAGSLGRMSFLAMWIFVPLMW 175
 DB 120 KGGGADALVETPVPWVPLYPMATVYVFCQVFAITLTLVAGSLGRMSFLAMWIFVPLMW 179
 QY 176 TFSYTVGAFSLWGGFLFHWGYIDYCGGYVIVHAGIAGFTAAVVGPPRAQKDRERFPN 235
 DB 180 TFSYTVGAFSLWGGFLFHWGYIDYCGGYVIVHSSGVAAGFTAAVVGPPRSTKDRERFPN 239
 QY 236 NIIFFTGTAGLLMAGAGFNGGFPYANSVAVANTNICTMSLIVWTCLDVIFPKKP 255
 DB 240 NVILMLTGAAILMAGAGFNGGDPYSANIDSILAVNTNICAATSLVWTCLDVIFPKKP 299
 QY 296 SVYGAVOGMITGLVCTTPAAGVQ 319
 DB 300 SVYGAVOGMITGLVCTTPAAGVQ 323

RESULT 11
 ABM90348
 ID ABM90348 standard; protein; 325 AA.
 AC ABM90348;
 XX 02-JUN-2005 (first entry)
 DT Rice abiotic stress responsive polypeptide SEQ ID NO:9070.
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:9070.
 KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX Oryza sativa.
 OS
 XX
 XX WO2003008540-A2.
 PN 30-JAN-2003.
 PD 21-JUN-2002; 2002WO-US019668.
 PF 22-JUN-2001; 2001US-0300112P.

PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 9070; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX Sequence 325 AA;
SQ
Query Match 53.6%; Score 1357; DB 7; Length 325;
Best Local Similarity 76.5%; Pred. No. 1.1e-121;
Matches 248; Conservative 30; Mismatches 40; Indels 6; Gaps 2;
QY 1 MESSATVPLVAGNTSASVADMLKGDNAQVLAATVGLGSPGLVVLGGVKKKAA 60
DB 1 MSGDANMSVAAYOPSGMA-VPEWLKNGDNAMQWISATLVGMSVPLVILYGSIVKKKAA 59
QY 61 VNSAFALAFAPAAVWICWTTAAVNSFGEKLPIMGKARPAADQGLVGRALPATVHY- 119
DB 60 VNSAFALAFAPAAVWICWTTAAVNSFGEKLPIMGKARPAADQGLVGRALPATVHY- 119
QY 120 ----RADGSVETAABEPLYPMATVVFQCVFAATILILVAGSLIGMSFLANMIFVPLWL 175
DB 120 KGGGADALVERPFWVPLYPMATVVFQCVFAATILILVAGSLIGMSFLANMIFVPLWL 179
QY 176 TTSYTYGASLWGGGLFPHMGVIDYGGGYIHVSAGIAGFTAAVWGPRAQKDRERFPN 235
DB 180 TFSYTYGASFLWGGGLFPHMGVIDYGGGYIHVSAGIAGFTAAVWGPSTXDRERFPN 239
QY 236 NLLFTLTGGLMAGAFNGGFPYANSVASMAVNTNICTMSLIWTCDDVIFKKXP 295
DB 240 NVLLMLTGLMAGAFNGGFPYANSVASMAVNTNICTMSLIWTCDDVIFKKXP 299
QY 296 SVVGAQGMITGLVCTTPAGVVO 319
DB 300 SVVGAQGMITGLVCTTPAGVVO 323
RESULT 12
ABM89810
ID ABM89810 standard; protein; 440 AA.
XX
XX ABM89810;
AC
XX 02-JUN-2005 (first entry)
XX
XX Rice abiotic stress responsive polypeptide SEQ ID NO:8056.
XX

KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX
XX Oryza sativa.
OS
XX WO2003008540-A2.
XX
XX
XX 30-JAN-2003.
XX
XX 21-JUN-2002; 2002MO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 8056; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX Sequence 440 AA;
SQ
Query Match 53.4%; Score 1352; DB 7; Length 440;
Best Local Similarity 63.1%; Pred. No. 5.1e-121;
Matches 253; Conservative 45; Mismatches 59; Indels 44; Gaps 4;
QY 106 LTVGRALPA-TVHYRADGSVETAABEPLYPMATVVFQCVFAATILILVAGSLIGMSF 164
DB 24 LTVGRALPA-TVHYRADGSVETAABEPLYPMATVVFQCVFAATILILVAGSLIGMSF 164
QY 165 LAMMIFVPLMIFSTYVGAFAFLMGGLFPHMGVIDYGGGYIHVSAGIAGFTAAVWGP 224
DB 78 KAMMAFVPLMIFSTYVGAFAFLMGGLFPHMGVIDYGGGYIHVSAGIAGFTAAVWGP 137
QY 225 AOKDRERFPNNILFTLGGGLMAGAFNGGFPYANSVASMAVNTNICTMSLIW 284
DB 138 SASDRERFPNNILFTLGGGLMAGAFNGGFPYANSVASMAVNTNICTMSLIW 197
QY 285 TGLDVIFFPKSPVAVAGMITGLVCTTPAA-----GVVGM--- 321
DB 198 TGLDVIFFPKSPVAVAGMITGLVCTTPAA-----GVVGM--- 321
QY 322 -----AALVWGLAGSIIPYTWMLHKRSKILQRYVDTLGVFTHGVAGIL 367
DB 258 LVCITTPGAGPBARLAIWGLISGSIIPYTWMLHKRSKILQRYVDTLGVFTHGVAGIL 317
QY 368 GGLTLGLFAEPFLCNLFPLVADSGAFYGGAGAFQGIAGGLFVVAAMVVVTSLICLA 427
DB 318 GGATYGLFAEPFLCNLFPLVADSGAFYGGAGAFQGIAGGLFVVAAMVVVTSLICIV 377

CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention

XX Sequence 476 AA;

Query March 27.4%; Score 693.5; DB 7; Length 476;

Best Local Similarity 36.4%; Pred. No. 1.4e-57;

Matches 170; Conservative 73; Mismatches 173; Indels 51; Gaps 10;

QY 2 SSSATVTVPLAYOGNTAS-----VADWLNKGDNAQLVATLVGLQSVGLVVLVGVVK 56

Db 45 SESVAVEELHDAAPAAAPAVAEAAAADRGDVAWMLSTLLVLMVVGALPFGGLVR 104

QY 57 KKMVNSAFMALYAPAAVVICVNTAAYNMSFGEKLLPTWKKRPPALDGLVGRALPRT 116

Db 105 SKNVLSVLSQILVFSVLVLLWVAAGYSAVFSAG-NPPEGS---FTEPAFLKG----- 153

QY 117 VHYRADGSVETAAVEPLVMATVVFQCVFAITLILVGLSLGMSFLAMWIFVPLMLT 176

Db 154 --FTPD-SVGNTPPIKGL-PDYLFVAFQSTFAGITTLALYGAFAEKIKFPAVLIFGALMFT 209

QY 177 FSYTVGAFSLMGSGFLFHWGVVIDYCGVYIVHSAGIAGFTAAVWVGPRAQKDERFPNN 236

Db 210 LSYIPMAHIVMGGYLIGELGALDPAGGVTHINAGVAGAMFVQKRLGQGTALPKPHN 269

QY 237 ILFTITGAGLLMGNAAGFVGSGPYAANSVSAVAVNTNICTMSLIVTCLDVIFFKPRS 296

Db 270 VFPTYIGMLVMVGFNAGSAAADYASLAFNTVLTATAAVALGWLTVSAIKGRFS 329

QY 297 VVGAQVQGITGLVCTTPAAGVVGMAALVGVLAGSIPWYTMILHKSKILQRYDDTLG 356

Db 330 ALGAASGAVAGLVGTTTPAGCTVGPGLAIVIGFVAGVVCWVGTL-----KLLKXDDTD 385

QY 357 VFHTGAVAGLLGGLTGLFAEPTLCNLFLPADSRGAFYGAAGAOFKQIAGLGV--- 413

Db 366 VFGVVGIGVIGAILTGVFSAQSL-----GGRKADLDIDAHQVWVQV 427

QY 414 -----VANNVVVTSLICLAINLLVPLRMDDKLEVGDDAV-HGEERY 454

Db 428 SVGLTVLMSAVVTAVILLVKKVVGRLVTEAERTGLDVTSHGESAY 474

RESULT 15

ABBS4938

ID ABBS4938 standard; protein; 413 AA.

XX ABBS4938;

AC 29-AUG-2003 (revised)

DT 16-MAY-2002 (first entry)

DE Lactococcus lactis protein amtb.

KM Bioynthesis; biodegradation; lactic bacterium; yogurt; cheese.

OS Lactococcus lactis; IL1403.

XX FR2807446-A1.

PN 12-OCT-2001.

PE 11-APR-2000; 2000FR-00004630.

PR 11-APR-2000; 2000FR-00004630.

PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;

XX WPI, 2002-043418/06.

XX New nucleotide sequence useful in the identification of Lactococcus

PT lactic and related species.

XX Claim 6; SEQ ID NO 1640; 2504pp; French.

PS The present invention is related to a Lactococcus lactis nucleotide

XX sequence (ABA90521) and related proteins (ABBS3300-ABBS5621). The nucleic

CC acid sequence is useful in the detection and/or amplification of nucleic

CC acid sequence, particularly to identify Lactococcus lactis or related

CC species. The proteins of the invention are useful for the biosynthesis or

CC biodegradation of a composition of interest. The invention helps research

CC in lactic bacteria, particularly useful in the production of yogurt and

CC cheese. Note: The sequence data for this patent is based on equivalent

CC patent WO200177334 (published 18-OCT-2001) which is available in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to

CC standardise OS field)

XX Sequence 413 AA;

QY 24 INKGDNAQLVATLVGLQSVGLVVLVGVKKKMAVNSAFMALYAPAAVVICVNTAY 83

Db 1 MDTSIAFTLICALVFLMT-PALAFYGLGRKRVNLTMMSLAPWALASILMIIGF 59

QY 84 NMSFGEKLLPTWKKRPPALDGLVGRALPRTVHYRADGSVETAAVEPLVMATV---- 139

Db 60 SFSFS-----GNSWIGDFHILFPMNGVDNAK-NSLPPANHIDGL 98

QY 140 -VYFQCVFAITLILVAGSLGRMSFLAMWIFVPLMLTFSYTVGAFSLMGSGFLFHWGV 198

Db 99 FSGFQMMISITVALITSSVVGKRFPTIILFMTAKLIVYVPLAHMWGGGFLAQHAI 158

QY 199 DYCGGVYIVHSAGIAGFTAAVWVGPRAQKDERFPNNILFTLTGAGLLMGNAAGFNGG 258

Db 159 DPAGGDVHHISSGVLGLALVLGKRDRYERLDYRPHNIPRVIGAGLLMFGMFGFNAGS 218

QY 259 PYAANSVSAVAVNTNICTMSLIVTCLDVIFFKKSVEVAGVQGITTPAAGV 318

Db 219 ALAANGVAINAFMTNTAAAAAAMFSMWIVKILIGKPSIVAGCSGAVVGLVATPAGAFV 278

QY 319 QGMAALVWGVLAGSIPWYTMILHKSKILQRYDDTLGVFHTGAVAGLLGGLTGLFAEP 378

Db 279 SUMSSLITGLVSPUSYFMISVKKK---LGYDADALAFGCHGIGMFGIMTGFATP 334

QY 379 TLCNLFLEPADSRGAFYGAAGAOFKQIAGLFPVANNVVVTSI---ICLAINLLVPL 434

Db 335 ALA-----PEKGYAAGLYGS-----GKLLANVSAVVFVIFTLVSWIILIKVIALFWPI 384

QY 435 RMPDDKLEVG-DDAVHGEERY 454

Db 385 RVSDBRAEAIGLDSEHEETAY 405

Search completed: July 22, 2006, 03:27:53

Job time : 201 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:28:11 ; Search time 41 Seconds
(without alignments)
1124.093 Million cell updates/sec

Title: US-10-713-648A-63

Sequence score: 2534
1 MESSATVPLVLAQGNISASV.....GEMVDYTKGSDPAANAVPVV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1682.5	66.4	475	2	T01260
2	985.5	38.9	509	2	G90257
3	722	28.5	412	2	C69188
4	717.5	28.3	442	2	C82985
5	706	27.9	423	2	H70310
6	691	27.3	431	2	AF0381
7	660	26.0	428	2	AC0560
8	659	26.0	433	2	AB3273
9	655.5	25.9	439	2	B75487
10	652	25.7	413	2	H86823
11	651.5	25.7	510	2	C87415
12	650.5	25.7	492	2	AB2632
13	650	25.7	428	2	E85542
14	650	25.7	428	2	C64775
15	650	25.7	428	2	A90692
16	640.5	25.3	407	2	A69188
17	637.5	25.2	404	2	A36865
18	635.5	25.1	434	2	C81927
19	633.5	25.0	477	2	H70747
20	632.5	25.0	434	2	E81177
21	621	24.5	449	2	H97689
22	621	24.5	449	2	AE2915
23	619	24.4	470	2	AE1930
24	591.5	23.3	401	2	AF1626
25	589.5	23.3	401	2	AD1264
26	589	23.2	416	2	A89996
27	582.5	23.0	448	2	T35667
28	574.5	22.7	391	2	A69372
29	569.5	22.5	405	2	H96983

30	567	22.4	388	2	D69468	ammonium transport
31	515	20.3	510	2	E82918	ammonium transport
32	513.5	20.3	512	2	T50244	probable ammonium
33	507.5	20.0	521	2	F82918	ammonium transport
34	506	20.0	499	2	S51089	ammonium transport
35	474.5	18.7	492	2	S46225	ammonium transport
36	451.5	17.8	489	2	S69027	ammonium transport
37	448.5	17.7	435	2	H72379	ammonium transport
38	425.5	16.8	421	2	B84129	ammonium transport
39	410.5	16.2	507	2	S76687	hypothetical prote
40	405	16.0	518	2	AD1930	ammonium transport
41	384	15.2	442	2	S74801	ammonium transport
42	372	14.7	468	2	A69468	ammonium transport
43	357	14.1	498	2	AC1930	ammonium transport
44	338.5	13.4	501	2	T06653	ammonium transport
45	337.5	13.3	514	2	T06585	ammonium transport

ALIGNMENTS

RESULT 1
T01260
probable ammonium transport protein P16M14.22 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: T01260; T02516; B84603
R/Rounaley, S.D.; Kaul, S.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.
submitted to the EMBL Data Library, July 1998
A/Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A/Reference number: Z14213
A/Accession: T01260
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-475 <R0U>
A/Cross-references: UNIPROT:Q9M6N7; UNIPARC:UPI0000048613; EMBL:AC003028; NID:G3335356; I
R/Rounaley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, August 1998
A/Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A/Reference number: Z14676
A/Accession: T02516
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-434 <R02>
A/Cross-references: UNIPARC:UPI0000178B16; EMBL:AC004683; NID:G3395421; PID:G3395443
A/Experimental source: cultivar Columbia
R/Rounaley, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, August 1998
A/Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A/Reference number: A84420; WUID:20083487; PMID:10617197
A/Accession: B84803
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-475 <STO>
A/Cross-references: UNIPARC:UPI0000048613; GB:AE002093; NID:G6598436; PIDN:AA28754.2; G
C/Genetics: A:Gene: Atg38290
A/Map position: 2
A/Intons: 104/3; 201/3; 297/1; 331/3
C/Superfamily: ammonium transporter nrgA
Query Match 66.4%; Score 1682.5; DB 2; Length 475;
Best Local Similarity 66.8%; Pred. No. 3.1e-121;
Matches 300; Conservative 61; Mismatches 77; Indels 11; Gaps 1;
QY 20 VADWLNKGNANQVAATLVGLQSVDPGLVLLYGCVVKKKMAVNSAFMAYAPAAVWICV 79
DB 12 VPEWLNKGNANQVAATLVGLQSVDPGLVLLYGCVVKKKMAVNSAFMAYAPAAVWICV 71
QY 80 TAAVYNSPGEKLLPIWGKARPALDGLVGRALPATVHYRADGSVETAVERPLYMATV 139

```
Db 72 LICYGMARCEBELLPERMGKGPAPFDGCVLKGAQKIF-----NSVNAAPYFPMAITL 120
Oy 140 VYFQCVPAATITLILVAGSLGRMSFLAMNI FVPLMTFSYTVGAPSLMGCGFLFHWGVID 199
Db 121 VYFQCVPAATITLILVAGSLGRMNIKAWMA FVPLMTLFSYTVGAVSIMWGGFLYOMGVID 180
Oy 200 YCGGVVHVSAGIAGTAAVYWGPRACKRERPPNNILFTLTGAGLLMGAGNFGGSP 259
Db 181 YSGGVVHVSAGIAGTAAVYWGPRACKRERPPNNILFTLTGAGLLMGAGNFGGSP 240
Oy 260 YAANSVSAVNAVNTNICTAMSLIWTCLDVIFFKKSPVAVAGOMITGLVCTTPAAGVQ 319
Db 241 YAANITSSIAVANTNLSAATSLTWTTLDVIFFGKRSVIGALQGMVGTGLAGVTPGAGLIQ 300
Oy 320 GMAALVMGYLAGSIPTWYTMILHKRSKILQVDDTLGVFHTGAVAGLLGGLTGLFAEPT 379
Db 301 TMAAIIIGVAGSTAPASWMIHKSALIQKVDTLAVFYTHAVVAGLLGGLTGLFAHPD 360
Oy 380 LCNLFPLVADSRGAFYGAAGAGQKQIAGGLFVYAMNVVNTSLCLATNLVPLRMPD 439
Db 361 LCVLVLPLPATGAFYGGNGKQQLKQLAGAFLIAYMNVSTTILILAIRVFLPLRMAE 420
Oy 440 KLEVGDDAVHGEBAVYALMGDGMVDYTKH 468
Db 421 ELGIGDDAHGEBAYALMGDGEKFDATRH 449
```

RESULT 2

```
G90257
ammonium transporter SSO1054 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90257
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozere, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Regan, M.A.; Sersen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-509 <KUR>
A:Cross-references: UNIPROT:Q97275; UNIPARC:UPI0000064334; GB:AE006641; NID:G13814242; E
C:Gene: SSO1054
C:Superfamily: ammonium transport protein
```

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Query Match 38.9%; Score 985.5; DB 2; Length 509;
Best Local Similarity 44.7%; Pred. No. 7, 1e-68;
Matches 203; Conservative 63; Mismatches 143; Indels 45; Gaps 8;

Oy 17 SASVADMLKGNAMQVLAATLVGLQSVPLVLYXGVVKKKMANVSAMFALYAFAPAVI 76
Db 56 AAASVSWLDTGSAMMLTATFVGLQSVPLVLYXGLSKKXAVNSALMIFAPAVI 115
Oy 77 CVATMAVNSFGEKLL-----PIWGKAPALDOGLVGRAL--PATYHYA 121
Db 116 IWIINGVSFGFYPALVSIHGYSIFGYPIPMWG-----GLFNASQTTYGSGAHAN- 166
Oy 122 DGSVERAAVEPLYPMAITVYFQCVFAATITLILVAGSLGRMSFLAMNIFVPLMTFSYTV 181
Db 167 -----LPTATTFIFQCVFAATITLILVAGSLGRMNFKAMNVVFPMSLLVYSP 214
Oy 182 GAFSLMGCGFLFHWGVIDYCGGVVHVSAGIAGTAAVYWGPRACKRERPPNNILFTL 241
Db 215 VAYWLPAGGWLMQLGAVDSGGVYHVDAGVGLAALAIIGPLASER-KLBAHSLPLVL 273
Oy 242 TGAGLLMGAGNFGGSPVAAASVAMVLTNTNICTAMSLIWTCLDVIFFKKSPVAVGAV 301
Db 274 VGAGLIMLGMDGNGDPLGATVDAAIAVLTNTNIATAVAVVWMLDMKRFGEKPTLIGAT 333
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Oy 302 QGMITGLVCTTPAAGVYVQGMALVMGYLAGSIPTWYTMILHKRSKILQVDDTLGVFHTH 361
Db 334 SGATITGLVAITPAGVYVQGMALIGIFSSIIPMALYWEK-----LRVDDTLGVFHTH 389
Oy 362 GVAGLIGGLTGLFAEPTLCNLFLPVADSRGAFYGAAGAGQKQIAGGLFVYAMNVVY 421
Db 390 GIAGVIGGLTGLVFPANFPAVYQFVAP--GLTGALYG--NWQLGIQALAAVIVFYVDFAIT 445
Oy 422 SLICLATNLVPLRMPDDKLEVGDDAVHGEBAVA 455
Db 446 FGLKFTGLFPLQAPQELAIQDYAHMGEBAVS 479
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RESULT 3

```
C69188
ammonium transporter - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: C69188
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
; Qiu, D.; Spadefora, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani, N.;
K.; S.; Church, G.M.; Daniels, C.U.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: C69188
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-412 <MTH>
A:Cross-references: UNIPROT:O26759; UNIPARC:UPI0000139B9C; GB:AE000846; GB:AE000666; NID:
A:Experimental source: strain Delta H
C:Genetics:
C:Gene: MTH663
C:Superfamily: ammonium transporter nrgA
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Query Match 28.5%; Score 722; DB 2; Length 412;
Best Local Similarity 36.6%; Pred. No. 8, 3e-48;
Matches 159; Conservative 74; Mismatches 169; Indels 32; Gaps 7;
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Oy 24 LNKGNAMQVLAATLVGLQSVPLVLYXGVVKKKMANVSAMFALYAFAPAVI 83
Db 10 LNSGDTAMMLVSTALVMTVPVGLFYGGLTKKENVLTNMFSLIAFAVSTIIVLYG 69
Oy 84 NMSFGEKLLPIWGKAPALDOGLVGRALPATYHYRADGSVERPAVEPLYPMAITVYFQ 143
Db 70 QPAPFADIMGFISGVNLMNMGVNTA-----AALAPITPDPFYIAFQ 113
Oy 144 CVFAATITLILVAGSLGRMSFLAMNIFVPLMTFSYTVGAPSLMGCGFLFHWGVIDYCGG 203
Db 114 LTFATITVALISGAVBERMKFSAMLAFLVLSLVYVVAHVMWGGFLAOLGALDFAGG 173
Oy 204 YVHVSAGIAGTAAVYWGPRACKRERPPNNILFTLTGAGLLMGAGNFGGSPVYAN 263
Db 174 TVVHINSVGAALAAVYLLGKR--KD--TRLPLNIGYSYIGASLLMFGFGFNAGSALTAG 230
Oy 264 SVASAVNAVNTNICTAMSLIWTCLDVIFFKKSPVAVAGOMITGLVCTTPAAGVQMAA 323
Db 231 GLAASAFVLTNTNIAAGVNSVIMDYLVKGRFVYLGISGAVAGVATTPAAGFTVYPA 290
Oy 324 LVMGYLAGSIPTWYTMILHKRSKILQVDDTLGVFHTGAVAGLLGGLTGLFAEPTLCNL 383
Db 291 LIIGVTSVISYLAVSYLKPR---LGYDDALDVGIGMGSIGSVATGLFAAPFINEL 346
Oy 384 FLPVADSRGAFYGAAGAGQKQIAGGLFVYAMNVVNTSLCLATNLVPLRMP--DDTLB 442
Db 347 -----GTGLLYGNB--QLTAQVIAVAVVAVSVVTLIIGKLDFTVGLVSGKEEWE 398
Oy 443 VGDDAVHGEBAVYAL 456
Db 399 GLDTHLHRETYRI 412
```

RESULT 4

C82985
ammonium transporter AmtB PA5287 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_rev15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C82985
R/Stover, C.K.; Pham, X.Q.; Ewitt, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: C82985
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-442 <STO>
A/Cross-references: UNIPROT:Q9HTR7; UNIPARC:UPI000000C5F8B; GB:AE004941; GB:AE004091; NID:A:Experimental source: strain PA01
C/Genetics:
A/Gene: amtB; PA5287
C/Superfamily: ammonium transporter nrgA

Query Match 28.3%; Score 717.5; DB 2; Length 442;
Best Local Similarity 36.7%; Pred. No. 2e-47;
Matches 170; Conservative 70; Mismatches 178; Indels 45; Gaps 10;

QY 7 VVPLAQNTSASVADWMLKKGDNAQVATLVGLQSVPGVLVLYGGVYKKKAAVSAPM 66
DB 12 LLSLALPGVALAEEBVLNSGDTAMMLISFALVLTITPGALFYGGMVAK-NVLSIMM 70
QY 67 ALYAFNA-WVICVNTAANNVSPG-----EKLPIWKGARPALDQGLLVGRALPATVHYRA 121
DB 71 QCFATIGLITLWVYVYSLAFPTAGMEKVLNFSVGGDLRAFLSG-----LTA 121
QY 122 DGSVETAAVEPLYPATVVFQCFAPATLTLVAGSLGRMSFLAMMIFVPLMTFSYTV 181
DB 122 DGLTSATNA--LPRESVITFFQMTFALITPALLVGAFAERMKFSAMLIFAVFTVYAP 178
QY 182 GAESLWG--GGFLPHMGVIDYCGGYVTHSAGIAGTAAYVGPRAQKREPPNNILF 239
DB 179 IAHMVNSGCGALMWDGVLDFAGGTVHHVAGIAGVACLVIGKRGYPTTPAPAPHLG 238
QY 240 TLTAGLILMMGAGFGGCGGYAANSVASMAVLNTNICTAMSLIWTCLDVIFFKPSVVG 239
DB 239 TLVGAALMLTGMWGFPAAGSAAANNGTRGMALVTOIATAAALAMPFAEITTHGKPSALG 238
QY 300 AVQGMITGLVCTTPAAGVVOGMALVWGLVAGSIPTWTMILHKRSKILQRPVDTLGVPH 359
DB 299 IASGVAGVATTPAAGTAGPMGALVIGLASSVTCFPAATSLKALK---YDSDLDFG 354
QY 360 THGVAGLGLGLTGLFAEPTLCNLFPLVADSRAFGAG-----GAQFSQIAGLGFV 414
DB 355 VHAVGVIGVALLTGIAPAASL-----GGFSGVSDIGAQFVQKGVAFV 399
QY 415 AMNVVYTSLICLAINLLVPLRMPDKEVG-DDAVHGEERYAL 456
DB 400 VYTAVTFTVLKVLDMGLRVEBEAVGLDLALHNERGYNL 442

RESULT 5
H70310
ammonium transporter - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_rev15-May-1998 #text_change 09-Jul-2004
C/Accession: H70310
R/Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy

A/Cross-references: UNIPROT:O66515; UNIPARC:UPI000005627E; GB:AE000674; NID:92982850; PII
A/Experimental source: strain VF5
C/Genetics:
A/Gene: amtB
C/Superfamily: ammonium transporter nrgA

Query Match 27.9%; Score 706; DB 2; Length 423;
Best Local Similarity 35.7%; Pred. No. 1.4e-46;
Matches 157; Conservative 78; Mismatches 157; Indels 48; Gaps 9;

QY 24 LKNGDNAQVATLVGLQSVPGVLVLYGGVYKKKAAVSAPMALYAFAAWICWTMAY 83
DB 25 LDQNTAMLVASALVFTVTPGLALFYGLDPSKSLNTIMSFSAFVLTITVFGV 84
QY 84 NNSFGKLLPIWGKARPALDQGLLVGRALPATVHYRADGSVETAAVEPLYPATVYQ 143
DB 85 SVAYGDIPIFGIGN-----PFOVLGKSGINSIDGYPLDLMTQ 126
QY 144 CVPAATLTLVAGSLGRMSFLAMMIFVPLMTFSYTVGAFSLMGGLPHMGVIDYCG 203
DB 127 LTFATITTLISGSFVGRKKFSAMILFALMSVFPVPAHWYGGGFLANDGALDPAQ 186
QY 204 YVHNSAGIAGTAAYVGPRAQKREPPNNILFTLGAQLMMGAGFGGCPYAN 263
DB 187 TVVHINAGIAGVGLIIGRR--KDTSLI-PNNVPLVALGAGILWPGMFGFNAGSALGAN 243
QY 264 SVASNAVLNTNICTAMSLIWTCLDVIFFPKRSVYCAVQGMITGLVCTTPAAGVQMAA 323
DB 244 ESAWAMAMITVYATSPALAMFTEWLHVGKPLVVGISGIVAGVATTPAAGFVNLGS 303
QY 324 LVWVAGSLIPWTMILHKRSKILQRPVDTLGVPHHAGLGLTGLFAEPTLCNL 383
DB 304 IFIGALA-SVCAPFWALVKKP--FGYDALDVEFIHGRIAGVAVLGVFADPNV--- 356
QY 384 FLVPADSRGAFYGAAGAQFGK-----QIAGGLFVANNVYTSLICLAINLLVPLR- 436
DB 357 -----GGTGLGLGNPKQVLIQIEGIATILVSALITAVILLVLRKAVGLRVS 404
QY 437 PDDKLEVGDAVHGEERYAL 456
DB 405 EBEELTEL-DSSLHGEKAYNL 423

RESULT 6
AF0381
probable ammonium transporter YPO3142 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_rev15-Nov-2001 #text_change 09-Jul-2004
C/Accession: AF0381
R/Farkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Farrugia, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AF0381
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-431 <KUR>
A/Cross-references: UNIPROT:Q8ZC80; UNIPARC:UPI000000DCE76; GB:AL590842; PIDN:CAC92377.1;
C/Genetics:
A/Gene: YPO3142
C/Superfamily: ammonium transporter nrgA

Query Match 27.3%; Score 691; DB 2; Length 431;
Best Local Similarity 35.3%; Pred. No. 2e-45;
Matches 157; Conservative 76; Mismatches 160; Indels 52; Gaps 9;

QY 19 SVADWINKGDNAQVATLVGLQSVPGVLVLYGGVYKKKAAVSAPMALYAFAAWICW 78
DB 28 AVAD--KADNAFMIMICTALVLFMTITPGALFYGLIRSKNVLSTMTQVWVSFALCVLM 84
QY 79 VTMANNMSFGKLLPIWGA-RPALDQGLLVGRALPATVHYRADGSVETAAVEPLYPMA 137

OY	63	SAPMALVFAAV-WICVTTAAYNMSFGKLLPIYMGKAPALDDGLVGRALLPATVHYRA	121
Db	106	SYMMQVSTVALIGFAMMLMGYSFAFTDG--GSMDKFVGGLGRVFLNG--VTPPS----	156
OY	122	DGSEVETAAVEPLYPMAVTVVYFQCVPAATITLLIVAGSLIGRMSFLAMMIFVPLMTFSYTV	181
Db	157	--NATFSTGVIPBELTIFIAFOSTPMAITALLVVGSLVERKKFAALVAFALMLPLLSYTP	214
OY	182	GAFSIM-----GGGFLEHMGVIDYCGSYVIHVSAGIAGFTAAVWGPR	225
Db	215	IAHMMWMMPGENAIALAPEDTVKSGLLWFGSLPAGCTVHINAGIALVGAITLGRQ	274
OY	226	QKDRERPPNNILFPLTGAGLLMMGAMGFGCGPAAASVASMVLNTNICTAMSLIYWT	285
Db	275	GCKEPMPPHSHLTLLVAGLLIWMGPGFNAGSNLESNGYSLAMVNTFIIATAGAGLSMT	334
OY	286	CLDVIFFKKPSVGAVMQMITGLVCITPAAGVVGMAALVNGVLAGSIPLYMTMILHKRS	345
Db	335	LVEWTRKKPSPALGLASGIVAGLVAVTPPAAGPAGPMGALITGLVSP-----CIIFCSV	390
OY	346	KILQKRVDDTLGVFRHGVAGLLGSLLTGLPAEPTLCNLFLEVADSRKAFYGGAG-----	399
Db	391	KNALKYDLSLAFGIHIGIVGALGTGLVNP-----WGAGVADYTS	435
OY	400	-----GAQFGKQIAGGLFVAVMNVVTSILCLAINLVPLRMPDDKLE	442
Db	436	CGKQDDLTCDPAVYDMGVQMLAKAVGVITLMSAINTALVFYITKIVIGRBAPEAE	495
OY	443	VG-DDAVHGEENY	454
Db	496	DGLDISEGERAY	508

RESULT 12

A82632 ammonium transporter XF1844 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: A82632

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82632

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-492 <SIM>

A:Cross-references: UNIPROT:Q9PCD7; UNIPARC:UPI00000C2857; GB:AE004005; GB:AE003849; NII

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reznach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B

R:Triones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, b

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Jungueira, M.L.; Kemper, E.L.; Kitzajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigry

chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Martino, C.L.; Marques M.V.; Martins, F

A:Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de M., de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1844

C:Superfamily: ammonium transporter nrgA

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QY 1 MSSATVPLAQGNTSASVADMLKNGDNAMQVATLTGLQSPGLVYLYGGVKKKMA 60
Db 64 MSEAPSPDAALPKTTPFPVVD--KGDVAMMLTSTLLVLMLVLPGLALTYGGALRSKNV 120
QY 61 VNSAFMALYAFAAVVICWVTWALYNNMSF--GEKLLPTWKGARPALDQGLVGRALPATVH 118
Db 121 LSIWQIGVWFSLIHLMLWLYGSLAFADGDMFIGFNKA-----FLYG----- 164
QY 119 YRADGSVETAVERPLY-----PMATVYFQCCFAAITLLVAGSLLGRRSFLAMTIFVP 172
Db 165 -----VDTATLADPFSKGFKLPEYLVAFFOLTFPAITGLVLGAFERKFAFVLLFIF 218
QY 173 LMLTSTYTGAFSLWG--GGFLFHWGVIDYCGGVIVSAGIAGFTAAVYWGSPRAQKDRER 231
Db 219 IWFSGCYLPRLAMWSTBFLSKGALDPAGGIVYVHINMGIADLVGAYFYGKXRFPGQOVA 278
QY 232 PPPNNILFTLGAGLLIMMGWAGFNGGGPYAANSVASMAVLNTNICTAMSLIWTCLDIYF 291
Db 279 VQPHNVPMFTFGALLLWVGWGFNGNAGSALENANSIALAFINTMLATPAALILVMSLSEKMT 338
QY 292 FKKBESVGAVQGMITGLVCIITPAAGVVOGMALIVMWLGSIMWYTMILHKSKIIOQV 351
Db 339 KGFSPALGASAMINGLVGITPAAGTVGPPGALAIQAVAAVCCIMGTGL---KRLIKV 394
QY 352 DDTLLGVFHTHGVAGLLGGLLTGLFAEPTLCNLTPLVPADSRKGAFFYGGAG--GAQFGHQI 407
Db 395 DDTLDFVFGVHGIGVIGALITGLVFTDKAL-----GGGVYAEGMTMSNQVM 439
QY 408 --AGGLFV-VAMNVVYVTSLICAINILVPLRMPDDKLENG--DVAVHGEENY 454
Db 440 IQAMVEGSIWVIGIVSLGVFLIVKLLFGIRVSEERREBLDTTSHGESAY 490

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RESULT 13
B55342
probable ammonium transporter amtB [imported] - Escherichia coli (strain O157:H7, substra
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E05542
R:Perma,N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: E05542
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <STO>
A:Cross-references: UNIPROT:P37905; UNIPARC:UPI0000125A44; GB:AE005174; NID:g12513316; P
A:Experimental source: strain O157:H7, substrain EDL933
C:Gene: amtB
C:Superfamily: ammonium transporter nrgA

Query Match 25.7%; Score 650; DB 2; Length 428;
Best Local Similarity 34.6%; Pred. No. 2, 8e-42;
Matches 154; Conservative 77; Mismatches 162; Indels 52; Gaps 10;

19 SVADMLNKGDNMOMVLAATLVGLQSVGLVVLVGGVKKKMAVNASFAMLYAFAAWICW 78
25 AVAD--KADNPFMMICTLVLEFMTIPGIALFPGGLIRGNVLSTMLTQVVTVPALVCILW 81
79 VTMVNMSEFGKILPIWGRKRPALDGLLVGRALPATVHYRADGSVE-TAAVEPLYPMA 137
82 VVYGSIAFGE-----GNPF--GNIMWLMLKNIELTAVMGSIQYI 121
138 TVVYVQCFAATLLIVAGSLGRMSFLAMTIVPLMTFTSYVGAFLMGGGGLFHHGV 197
122 HVA-FQGSFACITVGLIVGALERIRFSAVLLFVVVMLTSTYPIAHMVGGGGLASHGA 180
138 IDYCGGVYIHVAGAGFTAAVWVGRPAKDRERFPNNLLFTLTGAGLLMMGMGAFNGG 257
161 LDFAGGTIVHINAAIAGLVGATVIGKRVGPKGAEPHNLPMVFTGALLYITGMFGFVAG 240

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Oy 258 GPYAANSVSAVAALVNTNTCTFMSLLVTCDDVIFPFKPSVVGAVQGMITGLVCTTPAGV 317
Db 241 SAGTANEIALAIFNTVAVTAAALIGMTIFGEMALRGKRSLLGACSGAIAGLVGTAPAGY 300
Oy 318 VQGNAAALMGVLAQSIPIYTWMTLHKRSKILQRPDDTLGVPHTGAVGLLGGLLTGLFAE 377
Db 301 IGVGALLIIGVAGAGLAGMGVYTM-----KLLRRDDPCDVGAVGVGCIQCIWGTGLFAA 356
Oy 378 PTLGNLFLPVADSRGAFYGGAG---GAQFGQIAGL---FVAAWVYVTSILCLAINL 430
Db 357 SSL-----GGVFAEGVYTMGHQLIVQLESIAITIVMSGVAFIYKILADL 401
Oy 431 LVPLRMPDDKLEVGDDA-VHGEZAY 454
Db 402 TVGLRVPDEQEREGLDVNSHENAY 426

RESULT 14
C64775
ammonium transport protein amtB - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: C64775; S77645
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C64775
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-428 <BLAT>
A:Cross-references: UNIPROT:P37905; UNIPARC:UPI0000125444; GB:AEO00151; GB:U00096; NID:95433
A:Experimental source: strain K-12, substrain MG1655
R:van Heeswijk, W.C.; Hoving, S.; Molenaar, D.; Stegeman, B.; Kahn, D.; Westerhoff, H.V.
Mol. Microbiol. 21, 133-146, 1996
A:Title: An alternative PII protein in the regulation of glutamine synthetase in Escherichia coli.
A:Reference number: S77644; MUID:97000355; PMID:8843440
A:Accession: S77645
A:Molecule type: DNA
A:Residues: 1-428 <VNA>
A:Cross-references: UNIPARC:UPI0000125444; EMBL:U04029; NID:g1103922; PIDN:AAD14837.1; F000000000
A:Experimental source: strain K-12, substrain W3110
C:Genetic8:
A:Gene: amtB
C:Superfamily: ammonium transporter nrgA
C:Keywords: transmembrane protein; transport protein
F:10-26/Domain: transmembrane #status predicted <TM1>
F:17-23/Domain: transmembrane #status predicted <TM2>
F:67-83/Domain: transmembrane #status predicted <TM3>
F:123-139/Domain: transmembrane #status predicted <TM4>
F:149-165/Domain: transmembrane #status predicted <TM5>
F:188-204/Domain: transmembrane #status predicted <TM6>
F:248-264/Domain: transmembrane #status predicted <TM7>
F:279-295/Domain: transmembrane #status predicted <TM8>
F:301-317/Domain: transmembrane #status predicted <TM9>
F:339-355/Domain: transmembrane #status predicted <TM10>
F:378-394/Domain: transmembrane #status predicted <TM11>

Query Match 25.7%; Score 650; DB 2; Length 428;
Best Local Similarity 34.6%; Pred. No. 2.8e-42;
Matches 154; Conservative 77; Mismatches 169; Indels 52; Gaps 10;

Oy 19 SVADMLKGDNAQVLAATLVGLQSVPGLVVLVYGVGVKKRAVNSAFMAALYAPAAWICW 78
Db 25 AVAD---KADNAFWMTCTALVLFMTIPGIALFYGGILRGKVLISMLQVTVTFALVCILW 81
Oy 79 VTMAYNMSFGEGLPIPIWKARPALDQGLVGRALPARVHYRADGVSE-TAAVEPLYDMA 137
Db 82 VVYGVSLAFGE-----GNVNF-GNINWLMKNIETLIVMSGIYQYI 121
Oy 138 TVVVFQCVFAATITLLVAGSLIGRMSFLAMMI FVPLWLTFSYTVGAFSLMGGFLFTMGV 197

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Db      122 HVA-FQSGFACITVGLIGALAEKRFESALIFVVMVLSTYIPAHMMGGGLASHKA 180
Qy      198 IDYCGGYIYHSAGIAGEFAAYVWPBPAQKDEREPNNILPTLTCAGLLMMGAFNGG 257
Db      181 LDFAGGYVHHNPAALAGLVAGLIGKRGVFGKEAFKPHNLPMVFSTALTYIGMFENNG 240
Qy      258 GPYAANSVASMALVNTNICTAMSLIVWTCLDVYIFPKKPSVGVAGVQGMITGLYCITPAAGY 317
Db      241 SAGTANBEIAALAFVNTVVAATAALIGMIFGEHALBKGPSLLDACSAGIAGLVGVTBACG 300
Qy      318 VQGNALVWGLVAGSIIPWYTMMLHKRSKILQRYVDTLGVFTHGVAGLLGLLTGLFAE 377
Db      301 IGVGAGLIIGVAGIAGLVAGTMTL-----KRLLRVDDPCDVFVHGVCGIIVGCMITGIFPA 356
Qy      378 PTLGNLFLPVADSRGAFYGGAG--GAQFGKOIAGSL---FVAMNVVYTSILICLAINL 430
Db      357 SSL-----GGVFGAGVGTMGHQLVLQBSIAITIVSWGVAFIgyKLAIDL 401
Qy      431 LVPFLMPDDKLEVGDDA--VHGSEAY 454
Db      402 TVGLKVPBEOQEREGLDVNSHGSEAY 426

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RESULT 15
A90692
probable ammonium transporter ECG0505 [imported] - Escherichia coli (strain O157:H7, sube
C|Species: Escherichia coli
C|Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C|Accession: A90692
R|Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A|Reference number: A96929; WUID:21156231; PMID:11258796
A|Accession: A90692
A>Status: preliminary
A|Molecule type: DNA
A|Residues: 1-448 <HAX>
A|Cross-references: UNIPROT:P37905; UNIPARC:UP10000125A44; GB:BA000007; PIDD:BAB33928.1;
A|Experimental source: strain O157:H7, subclstrain RIMD 0509952
C|Genetics:
A|Gene: ECG0505
C|Superfamily: ammonium transporter nrgA

Query Match      25.7%; Score 650; DB 2; Length 428;
Best Local Similarity 34.6%; Pred. No. 2, 8e-42;
Matches 154; Conservative 77; Mismatches 162; Indels 52; Gaps 10;

QY      19 SVADWLKNGDNAMQLVAATLVGLQSYVGLVLVYGVAKKMAVNSAFMALYPAAWICW 78
       :|||:|||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      25 AVAD---KADNAPMMICTALVFMTITPGIALFVGGLIRGNVLSMLTQVTVPALVCILW 81
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||

QY      79 VTWAINMSGEGELPLPWGARPALDOGLVGRALPATVHYRADSGVE--TAAYEPLPMA 137
       82 VVYGSLSLAFGE-----GNPF-GNTINLMKLKNIELPAVNGSITYOI 121
       |||:::|||||:::|||||:::|||||:::|||||:::|||||

QY      138 TVVYFCQCPFAATLLIVAGSLIGRMSPFLAMMIFVPLMTFSYTVGAFTSLWGSGFLPTFMGV 197
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      122 HVA-FQGSACTVGLIIVALERIRFSAILFPVVVMILTSTYPIAHMWGGGLASHGA 180
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||

QY      198 IDYCGGYIHVSAGIAFTAAYAVGCPRAQDRERFPNNILFTLTGAGLIMMGWAGNGG 257
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      181 LDFAGGTVVHINAIALIGVALTGKRVGFGEKAEPFHNLPMWFTGALLIYIGWFGFNAG 240
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||

QY      258 GPYAANSVASMAVLNTNICTASLIWTCLDIVFFKKPSVGVAVQGMITGLVTCITPAAGV 317
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      241 SAGTNEINEIALAFVVTIVATAAIIIGMIFGBMALRGKPSILGCSCGIAGLVGTPACGY 300
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||

QY      318 VCGMALVWGVLAGSIPLYTMIMILHKRSKILORVDDTLGVFHTHGVAGLLGLTLGLEFAE 377
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      301 IGVGALLIIGVAVGLAGLWGVTML----KRLLRVDDPCDVFGVHGCVGICINTGITPA 356
       :|||:::|||||:::|||||:::|||||:::|||||:::|||||

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OY 378 PTLCHLFLPVADSRGAFYCGAG---GAQRKQIAGL---FVAMNVVYTSLICIAINL 430
DB 357 SSL-----GGVGFAGSVTNGHQLLVQLESIAITTVMSGVAFIGYKLADL 401
OY 431 LVPLRMPDDKLEVDDA-VHGEAY 454
DB 402 TVGLRVPEEQEREGLDVNSHENAY 426

Search completed: July 22, 2006, 03:33:42
Job time : 42 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:34:51 ; Search time 29 Seconds
(without alignments)
952.519 Million cell updates/sec

Title: US-10-713-648A-63

Perfect score: 2534
Sequence: 1 MSSSATVPLAYOGNTSASV.....GEMVDTKKGSDAAVAPVV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA.New.*

1: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2534	100.0	479	US-10-713-648A-63	Sequence 63, Appl
2	2527	99.7	479	US-10-449-902-5313	Sequence 5313, A
3	1931	76.2	369	US-10-449-902-4731	Sequence 4731, A
4	1714	67.6	486	US-10-449-902-4317	Sequence 4317, A
5	1693.5	66.8	497	US-10-449-902-35281	Sequence 35281, A
6	1682.5	66.4	475	US-10-953-349-10298	Sequence 10298, A
7	1647	65.0	419	US-10-449-902-39814	Sequence 39814, A
8	1569.5	61.9	440	US-10-953-349-10299	Sequence 10299, A
9	1472.5	58.1	418	US-10-953-349-10300	Sequence 10300, A
10	1003.5	39.6	255	US-10-953-349-17239	Sequence 17239, A
11	951	37.5	304	US-10-449-902-54997	Sequence 54997, A
12	881	34.8	218	US-10-953-349-17240	Sequence 17240, A
13	845	33.3	208	US-10-953-349-17241	Sequence 17241, A
14	769	30.3	219	US-10-449-902-40126	Sequence 40126, A
15	589	23.2	428	US-10-471-571A-244	Sequence 244, App
16	547	21.6	486	US-11-185-301-2	Sequence 2, Appl1
17	530	20.9	524	US-10-449-902-49921	Sequence 49921, A
18	474.5	18.7	492	US-11-251-208-73	Sequence 24, Appl
19	344.5	13.6	507	US-11-296-657-24	Sequence 25, Appl
20	343.5	13.6	518	US-11-296-657-25	Sequence 26, Appl
21	337.5	13.3	514	US-11-296-657-23	Sequence 27, Appl
22	329	13.0	496	US-11-296-657-26	Sequence 22, Appl
23	327.5	12.9	513	US-11-296-657-27	Sequence 33, Appl
24	326	12.9	514	US-11-296-657-22	
25	325.5	12.8	519	US-11-296-657-33	

26	323	12.7	496	US-10-449-902-38313	Sequence 38313, A
27	313.5	12.4	500	US-11-251-208-447	Sequence 447, App
28	305	12.0	484	US-11-296-657-32	Sequence 32, Appl
29	301	11.9	488	US-11-296-657-30	Sequence 30, Appl
30	297	11.7	498	US-11-296-657-34	Sequence 34, Appl
31	291.5	11.5	498	US-10-449-902-51990	Sequence 51990, A
32	291.5	11.5	498	US-11-296-657-31	Sequence 31, Appl
33	291.5	11.5	532	US-11-296-657-28	Sequence 28, Appl
34	291.5	11.5	532	US-11-296-657-29	Sequence 29, Appl
35	276.5	10.9	492	US-10-449-902-36776	Sequence 36776, A
36	115.5	4.6	189	US-10-992-149-11	Sequence 11, Appl
37	111.5	4.4	500	US-10-449-902-28844	Sequence 28844, A
38	111.5	4.4	643	US-10-471-571A-4394	Sequence 4394, Ap
39	109	4.3	656	US-10-449-902-45299	Sequence 45299, A
40	103.5	4.1	443	US-11-056-3558-18881	Sequence 18881, A
41	103.5	4.1	487	US-11-056-3558-18880	Sequence 18880, A
42	103.5	4.1	955	US-10-449-902-41322	Sequence 41322, A
43	102.5	4.0	427	US-11-056-3558-18882	Sequence 18882, A
44	102.5	4.0	459	US-10-471-571A-472	Sequence 472, App
45	102.5	4.0	1052	US-10-497-088-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-713-648A-63
Sequence 63, Application US/10713648A
Publication No. US20060107344A1
GENERAL INFORMATION:
APPLICANT: POSCO
APPLICANT: POSTECH
APPLICANT: An, Gynheung
APPLICANT: Ryu, Choong-Hwan
APPLICANT: Han, Jong-Jin
APPLICANT: Kang, Hong-Gyu
APPLICANT: An, Kyungsok
TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
FILE REFERENCE: 20010-04USA
CURRENT APPLICATION NUMBER: US/10/713,648A
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/427,166
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 479
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
OTHER INFORMATION: line 1C-109-35 polypeptide sequence
US-10-713-648A-63
Query Match 100.0%; Score 2534; DB 6; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-198;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSATVPLAYOGNTSASVADWLNKGDNAWQVLAATLVGLQSPGLVVLXGVAKKKWA 60
DB 1 MSSSATVPLAYOGNTSASVADWLNKGDNAWQVLAATLVGLQSPGLVVLXGVAKKKWA 60
QY 61 VNSAFMALVFAFAVWICMTWAVNMSFGKLLPIWGKARPALDQGLVGRAPATVHYR 120
DB 61 VNSAFMALVFAFAVWICMTWAVNMSFGKLLPIWGKARPALDQGLVGRAPATVHYR 120
QY 121 ADGSEVTAAVEPLYPNATVYVFOCVFAATLILVAGSLGRMSFLAMITVPLMLTSSYT 180
DB 121 ADGSEVTAAVEPLYPNATVYVFOCVFAATLILVAGSLGRMSFLAMITVPLMLTSSYT 180
QY 181 VGNFSLMGSGFLFRWGVIVDCCGVVHVSAGIAGFTAAVWVGPRAQDRRFPNNILFT 240

Db 181 VQAFSLMGGGFLPHMGVIDYCGGYVHVSAGIAGFAAAYWVGPRAGKXDERPENNILFT 240
Qy 241 LTGAGLLMGMAGFNGGGGYAANSVASMAVLTNTICTASMLIWTCLDVIFFKKSUVGA 300
Db 241 LTGAGLLMGMAGFNGGGGYAANSVASMAVLTNTICTASMLIWTCLDVIFFKKSUVGA 300
Qy 301 VQGMITGLVCITPAGVVGMAALVWGVLAGSIPWYTMWILHKRSKILORVDDTLGVFPT 360
Db 301 VQGMITGLVCITPAGVVGMAALVWGVLAGSIPWYTMWILHKRSKILORVDDTLGVFPT 360
Qy 361 HGVAGLLGGLLTGLFAEPTLCNLFPLVADSRGAFYGAAGAGFGKQIAGGLFVVAANVV 420
Db 361 HGVAGLLGGLLTGLFAEPTLCNLFPLVADSRGAFYGAAGAGFGKQIAGGLFVVAANVV 420
Qy 421 TSLICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAVAAPVV 479
Db 421 TSLICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAVAAPVV 479

RESULT 2

US-10-449-902-53313
; Sequence 53313, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 53313
; LENGTH: 479
; TYPE: PRF
; ORGANISM: Oryza sativa
US-10-449-902-53313

Query Match 99.7%; Score 2527; DB 6; Length 479;

Best Local Similarity 99.6%; Pred. No. 7.7e-198;

Matches 477; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSSATVVEFLAYQGNTSASVADMLNKGDANMOLVAATLVGLOSVPGLVVLGGVVKKKMA 60
Db 1 MSSATVVEFLAYQGNTSASVADMLNKGDANMOLVAATLVGLOSVPGLVVLGGVVKKKMA 60
Qy 61 VNSAFNALYAFPAWVICWTWYNNMSFGEKLPIMWKARPAIDQGLLVRAALPATVHR 120
Db 61 VNSAFNALYAFPAWVICWTWYNNMSFGEKLPIMWKARPAIDQGLLVRAALPATVHR 120
Qy 121 AGGSVETAVERPIYPAATVYVFCVPAATLLIVASSLGRMSFLAMTIVPLMLTFSTT 180
Db 121 AGGSVETAVERPIYPAATVYVFCVPAATLLIVASSLGRMSFLAMTIVPLMLTFSTT 180
Qy 181 VQAFSLMGGGFLPHMGVIDYCGGYVHVSAGIAGFAAAYWVGPRAGKXDERPENNILFT 240
Db 181 VQAFSLMGGGFLPHMGVIDYCGGYVHVSAGIAGFAAAYWVGPRAGKXDERPENNILFT 240
Qy 241 LTGAGLLMGMAGFNGGGGYAANSVASMAVLTNTICTASMLIWTCLDVIFFKKSUVGA 300
Db 241 LTGAGLLMGMAGFNGGGGYAANSVASMAVLTNTICTASMLIWTCLDVIFFKKSUVGA 300
Qy 301 VQGMITGLVCITPAGVVGMAALVWGVLAGSIPWYTMWILHKRSKILORVDDTLGVFPT 360
Db 301 VQGMITGLVCITPAGVVGMAALVWGVLAGSIPWYTMWILHKRSKILORVDDTLGVFPT 360

Qy 361 HGVAGLLGGLLTGLFAEPTLCNLFPLVADSRGAFYGAAGAGFGKQIAGGLFVVAANVV 420
Db 361 HGVAGLLGGLLTGLFAEPTLCNLFPLVADSRGAFYGAAGAGFGKQIAGGLFVVAANVV 420
Qy 421 TSLICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAVAAPVV 479
Db 421 TSLICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAVAAPVV 479

RESULT 3

US-10-449-902-47331
; Sequence 47331, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 47331
; LENGTH: 369
; TYPE: PRF
; ORGANISM: Oryza sativa
US-10-449-902-47331

Query Match 76.2%; Score 1931; DB 6; Length 369;

Best Local Similarity 99.7%; Pred. No. 1.6e-149;

Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 115 ATVHYRADGSVETAVERPIYPAATVYVFCVPAATLLIVAGSLGRMSFLAMTIVPLM 174
Db 5 ATVHYRADGSVETAVERPIYPAATVYVFCVPAATLLIVAGSLGRMSFLAMTIVPLM 64
Qy 175 LTFSTYVGAFLMGGGFLPHMGVIDYCGGYVHVSAGIAGFAAAYWVGPRAGKXDERP 234
Db 65 LTFSTYVGAFLMGGGFLPHMGVIDYCGGYVHVSAGIAGFAAAYWVGPRAGKXDERP 124
Qy 235 NNILFTLTCAGLLMGMAGFNGGGGYAANSVASMAVLTNTICTASMLIWTCLDVIFFK 294
Db 125 NNILFTLTCAGLLMGMAGFNGGGGYAANSVASMAVLTNTICTASMLIWTCLDVIFFK 184
Qy 295 PSVGAAGVGMITGLVCITPAGVVGMAALVWGVLAGSIPWYTMWILHKRSKILORVDDT 354
Db 185 PSVGAAGVGMITGLVCITPAGVVGMAALVWGVLAGSIPWYTMWILHKRSKILORVDDT 244
Qy 355 LCVFTHGVAAGLLGGLLTGLFAEPTLCNLFPLVADSRGAFYGAAGAGFGKQIAGGLFV 414
Db 245 LCVFTHGVAAGLLGGLLTGLFAEPTLCNLFPLVADSRGAFYGAAGAGFGKQIAGGLFV 304
Qy 415 ANNVAVTSICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAV 474
Db 305 ANNVAVTSICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAV 364
Qy 475 APVVV 479
Db 365 APVVV 369

RESULT 4

US-10-449-902-43179
; Sequence 43179, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.

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; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43179
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-43179

Query Match      67.6%; Score 1714; DB 6; Length 486;
Best Local Similarity 69.0%; Pred. No. 9.1e-132;
Matches 319; Conservative 51; Mismatches 82; Indels 10; Gaps 4;

QY 10 LAYQNTSAS--VADMLKGNAMQVLAATLVGLQSVGLVYVYGGVKKKMAVNSAFM 66
DB 1 MAAAGAYSASLPVPDMLKGNAMQVLAATLVGLQSMFGLVYVYGGVKKKMAVNSAFM 60
QY 67 ALYAFAMVICWVTMAVYNNMFGKELPIWKGARPALDQGLVGRALPATVHYRADGSVE 126
DB 61 ALYAVASLLVWVTVGFBRMAGDQGLLPFGKAGVALLQSVLVGRATLPATM-----GAI- 115
QY 127 TAAVEPLYMATVYVYQCFAATLTLLVAGSLIGRMSFLAMMIFVPLMLTFSTYVAGFSL 186
DB 116 -PRTEPFYEPATLVLPQFEPAITLVLAGSVIGRMNIKAMWAFPLMLLSYVGAFFSL 174
QY 187 MGGGFPHNGVIDYCGGYVHVHVSAGIAGFAAYVWVGPRADKDERPFPNNILFTLGAGL 246
DB 175 MGGGFYRNGVIDYSGGYVYHLSGAGIAGFAAYVWVGPRADKDERPFPNNILFTLGAGL 234
QY 247 LWMGAGFNGGGRPYAANSVAMVLTNTICTAMSLVWTCLDVIFPKKPSVGAVOGMIT 306
DB 235 LWMGAGFNGGGRPYAANSVAMVLTNTICTAMSLVWTCLDVIFPKKPSVGAVOGMIT 294
QY 307 GLVCIIPAGGVVGMALVWGLAGSIPTVMTMILHKSKILORVDDTLGVFHTHGVAGL 366
DB 295 GLVCIPGAGLVQVTMAVWVGIFAGSVPMFTMMILHKSKALMKVDTLAVFHTHAGL 354
QY 367 LGGILGLFAEPTLCULFVADSRGAFYGGAGAGQKQIAGGLFVMAVNVVTSILCL 426
DB 355 LGGILGLLATPPLFSLSESTVPGLRGAFYGG-GIKQIGQLGGAAFVIAVNLVTTAILL 413
QY 427 AINILVPLRMPDLEVDGDAVGEAEAYALMGDEMYDVTKH 468
DB 414 GIGLFFPLRMPDQGLMIGDAAHGEAEAYALMGDEKFDARH 455

RESULT 5
; Sequence 35281, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
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; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35281
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-35281

Query Match      66.8%; Score 1693.5; DB 6; Length 497;
Best Local Similarity 67.9%; Pred. No. 4.3e-130;
Matches 305; Conservative 54; Mismatches 89; Indels 1; Gaps 1;

QY 19 SVADMLKGNAMQVLAATLVGLQSVGLVYVYGGVKKKMAVNSAFMALYAPAAWICM 78
DB 16 AVPAMLKGDITMQLAATFVGLQSMFGLVYVYGGVKKKMAVNSAFMALYASTLIW 75
QY 79 VYVYNNMFGKELPIWKGARPALDQGLVGRALPATVHYRADGSVEETAPEPLYPMAT 138
DB 76 VLVGFPRMAGDRLPFWAKAGPALDQGLVQRAVFPATAHYSGDGLTETPRTEPFYAEAA 135
QY 139 VYVYQCFAATLTLLVAGSLIGRMSFLAMMIFVPLMLTFSTYVAGFSLMGGFLLFWGYI 198
DB 136 LVLPFEFEPAITLVLAGSVIGRMNIKAMWAFPLMLLSYVYVGAFFSLMGGFLLYQMGYI 195
QY 199 DYCGGYVHVHVSAGIAGFAAYVWVGPRADKDERPFPNNILFTLGAGLWMGAGFNGCG 258
DB 196 DYSGGYVYHLSGAGIAGFAAYVWVGPRADKDERPFPNNILFTLGAGLWMGAGFNGCGA 255
QY 259 PYAANSVAMVLTNTICTAMSLVWTCLDVIFPKKPSVGAVOGMITGLVCITPAAGV 318
DB 256 PYAPNTATVAVLNTVNSATSLTWTCLDVIFPKKPSVGAVOGMITGLVCITPAAGV 315
QY 319 QGMAALVWGLAGSIPTVMTMILHKSKILORVDDTLGVFHTHGVAGLGLLGLTGFAB 378
DB 316 HTWSAMLMGMFAGSVPMFTMMILHKSKITLKVDDTLAVFHTHAGVAGLGLVTLGFATP 375
QY 379 TFCNLFVADSRGAFYGGAGAGQKQIAGGLFVMAVNVVTSILCLAINLPLRMPD 438
DB 376 ELCAIDCPLPNNRGVYV-SSGIGQLGKQGLAFVYVWMLVITSAILLCLGFLPLRMD 434
QY 439 DKLEVDDAVHGEAEAYALMGDEMYDVTK 467
DB 435 DQLMIGDDAAHGEAEAYALMGDEKFDVTR 463

RESULT 6
; Sequence 10298, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10298
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-10298

Query Match      66.4%; Score 1682.5; DB 6; Length 475;
Best Local Similarity 66.8%; Pred. No. 3.2e-129;
Matches 300; Conservative 61; Mismatches 77; Indels 11; Gaps 1;

QY 20 VADMLKGNAMQVLAATLVGLQSVGLVYVYGGVKKKMAVNSAFMALYAPAAWICM 79
DB 12 VPEMLKGNAMQVLAATLVGLQSMFGLVYVYGGVKKKMAVNSAFMALYAPAAWICM 71
QY 80 TAAVYNNMFGKELPIWKGARPALDQGLVGRALPATVHYRADGSVEETAPEPLYMATV 139
```

Db 72 LICYMARBEELLPEFGKGGPAFDGQYLKGAQIP-----NSNVAAPYFPMATL 120
Qy 140 VYFOCVPAITLILVAGSLGRMSFLAMNI FVPLMTESYTVGASLWGGFLPHKGVID 199
Db 121 VYFOCTFAITLILVAGSVLGRMNIAKAMNA FVPLMTIFSYTVGANSIMWGGFLYQWGVID 180
Qy 200 YGGGVYIHVSAGIAGTAAYWVGPRAKDRERPPNNIIFLTGAGLLMGMAGFPGGPR 259
Db 181 YGGGVYIHSSVAGFVAAYWVGPRKADREPPNNVLLMAGLMMGMSGRNGGAP 240
Qy 260 YAANSVAMVANTNICTAMSLIWTCLDVIFPKKPSVVGAVQGMITGVCITPAAGVQ 319
Db 241 YAANTSSIAVANTNLASAATSLIWTLLDVIFPKKPSVIGALQGMVGTAGVTPGAGLIQ 300
Qy 320 GHAALVMGVLASIPYTMILHKSKILQVDDTLGVHTHGVAGLGGLLTGFAERT 379
Db 301 TMAAIIIGVSGTAPWASMMIHKKSALQKVDTLAVFYTHAVAGLLGGIMTGJFAHD 360
Qy 380 LCNLFPLVADSRGAFVGAGAGQFGKQIAGSLFVYAMNVVTSLICLAIVLPLRMPD 439
Db 361 LCVLVLPLPATITGAFYGGNGKQLKQLAGAFAIVAMNVSTIILAIRVFIPLMAEE 420
Qy 440 KLEVGDDAVHGEBAVALMGDGEYDVTKH 468
Db 421 ELGIGDDAHGEEAVALMGDGEKFDATRH 449

RESULT 7
US-10-449-902-39814
; Sequence 39814, Application US/10449902
; Publication No. US20060123505A1

GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 39814
; LENGTH: 419
; TYPE: PRT
; ORGANISM: *Oryza sativa*
US-10-449-902-39814

Query Match 65.0%; Score 1647; DB 6; Length 419;
Best Local Similarity 72.2%; Pred. No. 2, 2e-126;
Matches 291; Conservative 52; Mismatches 60; Indels 0; Gaps 0;

Qy 66 MALVPAANWICWMAVYMSFGEKLLPTWKGARPLDGLVGRALPATYHVRADGV 125
Db 1 MALVFAAAMWICWMAVYMSFGDRLLPWKARPLDGLVGRALPATYHVRADGV 60
Qy 126 ETAATVEPLVPMATVYFOCVPAITLILVAGSLGRMSFLAMNIFVPLMTESYTVGAS 185
Db 61 EAPMLKPLVPAITVYFOCVPAITLILVAGSLGRMNIAKAMNAFVPLMTESYTVGAS 120
Qy 186 LMGGGFLPHWGVIDYCGGVYIHVSAGIAGTAAYWVGPRAKDRERPPNNIIFLTGAG 245
Db 121 LMGGGFLFQWGVIDYSGGVYIHSSGIAGLTAAYWVGPRASADREPPNNIILVLVAG 180
Qy 246 LLMGMAGNGGCPAANVASMAYLNTNICTAMSLIWTCLDVIFPKKPSVVGAVQGM 305
Db 181 LLMGMAGNGGCPAANVASMAYLNTNICTAMSLIWTCLDVIFPKKPSVVGAVQGM 240

Qy 306 TGLVCTPAGVQGMALVWGLAGSI PMYTMILHKSKILQVDDTLGVHTHGVAG 365
Db 241 TGLVCTITGAGLVQGMALVWGLAGSI PMYTMILHKSKEMQIDITLGVHTHGVAG 300
Qy 366 LGGGLLTGLFAEPTLCNLFPLVADSRGAFYGGAGAGQFGKQIAGSLFVYAMNVVTSLIC 425
Db 301 FLGATGTGLFAEPTLCNLFPLSIPDSKAFYGGGPGSGQFGKQIAGLFTYAMNIVITSITC 360
Qy 426 LAIVLPLRMPDDTLGVHTHGVAGLGGLLTGFAERT 468
Db 361 VILSLPLRIADDELIGDDAHGEEAVALMGDGEKFDATRH 403

RESULT 8
US-10-953-349-10299
; Sequence 10299, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953, 349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patencin version 3.3
; SEQ ID NO 10299
; LENGTH: 440
; TYPE: PRT
; ORGANISM: *Arabidopsis thaliana*
US-10-953-349-10299

Query Match 61.9%; Score 1569.5; DB 6; Length 440;
Best Local Similarity 65.6%; Pred. No. 4, 5e-120;
Matches 279; Conservative 60; Mismatches 75; Indels 11; Gaps 1;

Qy 44 VGLVVLVGVGVKKKMAVNSAFMALYAPAAWICWYTAAYMSFGEKLLPTWKGARPLD 103
Db 1 MGVLIIVLASIVKKKMAVNSAFMALYAPAAVLLCVLLCYMARBEELLPEFGKGGPAFD 60
Qy 104 OGLVGRALPATYHVRADGSVETRAVEPLYPMATVYFOCVPAITLILVAGSLGRMS 163
Db 61 OGYLKGAKIP-----NSNVAAPYFPMATLVYFOCTFAITLILVAGSVLGHMN 109
Qy 164 FLAMNIFVPLMTESYTVGAFSLWGGFLPHKGVIDYCGGVYIHVSAGIAGTAAYWGP 223
Db 110 IKAMNAFVPLMTIFSYTVGAFSLWGGFLYQWGVIDYSGGVYIHSSVAGFVAAYWGP 169
Qy 224 RAQKDRERPPNNIIFLTGAGLLMGMAGFNGGCPAANVASMAYLNTNICTAMSLIV 283
Db 170 RPKADREPPNNVLLMAGSLMGMAGFNGGCPAANVASMAYLNTNICTAMSLIV 229
Qy 284 WTCUDVIFPKKPSVVGAVQGMITGLVCTTPAAGVQGMALVWGLAGSI PMYTMILHK 343
Db 230 WTTLDVIFPKKPSVIGALQGMVGTAGVTPGAGLIQTMAAIIIGVSGTAPWASMMIHK 289
Qy 344 RSKILQVDDTLGVHTHGVAGLGGLLTGFAERTLCNLFPLVADSRGAFYGGAGQF 403
Db 290 KSAIQKVDTLAVFYTHAVAGLLGIMTGJFAHDLCVLPATITGAFYGGAGQF 349
Qy 404 GKQIAGSLFVYAMNVVTSLICLAIVLPLRMPDDKLEVDVHGEBAVALMGDGEY 463
Db 350 LKQLAGAFAIVAMNVSTIILAIRVFIPLMAEEELIGDDAHGEEAVALMGDGEK 409
Qy 464 DVTKH 468
Db 410 DATRH 414

RESULT 9
US-10-953-349-10300
; Sequence 10300, Application US/10953349
; Publication No. US20060107345A1

GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10300
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10300

Query Match 58.1%; Score 1472.5; DB 6; Length 418;
Best Local Similarity 65.0%; Pred. No. 3.3e-112;
Matches 262; Conservative 57; Mismatches 73; Indels 11; Gaps 1;

QY 66 MALYAPAAWICWYTAAYNMSFGEKLLPIWGKARPALDGLVGRALPATVHYRADGSV 125
DB 1 MALYAPAAWICWYTAAYNMSFGEKLLPIWGKARPALDGLVGRALPATVHYRADGSV 49

QY 126 ETAABEPLVPMATVYFQCVFAAITLLVAGSLIGRMSFLAMNIFVPLMTFSYTVGAFS 185
DB 50 NSNVAAPIYFMATLVYFQFTFAITTLVAGSVLGRNITAKMAFVPLMLIFSTTVGAYS 109

QY 186 LMGGGLFHWGVIDYCGGYIHSVAGIAGTAAYWGPRAQKDRERPPNNILFTLTGAG 245
DB 110 IMGGGLFYQGVVIDYSGGYIHLSSGAVGAAYWGPRAQKDRERPPNNILFTLTGAG 169

QY 246 LLMGAAAGNGGGPYAANSVASMALNTNICTAMSLIVTCLDIYIFPKKSVGAVOGMT 305
DB 170 LMMGSGFNGGAPYANLTSIAVLNTNLSAATSLVMTLVDIYIFPKKSVGALQGMV 229

QY 306 TGLVCTTPAAGVQGAALWGVLAGSIPWTMMIILHKRSKILQVVDITGVPHTHGAVG 365
DB 230 TGLAGVTPGAGLQTMVAIITIGVSGTAPWASMTIHKKSALQKVDITLAVFTTHAVAG 289

QY 366 LLOGLLTGLFAEPPTLCNLFLPVADSRCAPYGAAGAGOFQKQIAGGLFVAVMNVVTSLIC 425
DB 290 LLOGIMTGLFAHDLCLVLPPLPTRGAFYGGNGKQLKQLAGAAFIAMNVVSTTIL 349

QY 426 LAINLVPLRMPDDKLEVGDDAVHGEBAVYALMGDEMYDVTKE 468
DB 350 LAIRVFPILRMBEELGIGDDAAHGEBAVYALMGDEKFDATRH 392

RESULT 10
US-10-953-349-17239
; Sequence 17239, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17239
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-17239

Query Match 39.6%; Score 1003.5; DB 6; Length 255;
Best Local Similarity 72.7%; Pred. No. 2.5e-74;
Matches 184; Conservative 24; Mismatches 44; Indels 1; Gaps 1;

QY 9 PLAYQGTASVADMILKGNAMQVLAATLVGLQSVGLVTVYGGVYKKKMAVNSAFMAL 68
DB 1 PLAYQGTASVADMILKGNAMQVLAATLVGLQSVGLVTVYGGVYKKKMAVNSAFMAL 68

DB 4 PTAYQEHLPAS -PHMLNKGDNAWQVLAATLVGLQSMGLVILYASWYKKKMAVNSAFMAL 62

QY 69 YAPAAWICWYTAAYNMSFGEKLLPIWGKARPALDGLVGRALPATVHYRADGSVETA 128
DB 63 YAPAAWICWYTAAYNMSFGEKLLPIWGKARPALDGLVGRALPATVHYRADGSVETA 122

QY 129 AVEPLVPMATVYFQCVFAAITLLVAGSLIGRMSFLAMNIFVPLMTFSYTVGAFSLMG 188
DB 123 TSEPLFATASLVYFQFTFAITTLVAGSVLGRNITAKMAFVPLMLIFSTTVGAFSLMG 182

QY 189 GGFLLFWGVIDYCGGYIHSVAGIAGTAAYWGPRAQKDRERPPNNILFTLTGAGLLW 248
DB 183 GGFLLFWGVIDYCGGYIHLSSGAVGAAYWGPRAQKDRERPPNNILFTLTGAGLLW 242

QY 249 MGWAGNGGGPYA 261
DB 243 MGWAGNGGGPYA 255

RESULT 11
US-10-449-902-54997
; Sequence 54997, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54997
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54997

Query Match 37.5%; Score 951; DB 6; Length 304;
Best Local Similarity 69.1%; Pred. No. 5.6e-70;
Matches 170; Conservative 27; Mismatches 49; Indels 0; Gaps 0;

QY 19 SVADMLNKGDNAWQVLAATLVGLQSVGLVTVYGGVYKKKMAVNSAFMALYAPAAWICW 78
DB 20 AVPAWLNKGDNAWQVLAATLVGLQSMGLVILYASWYKKKMAVNSAFMALYAPAAWICW 79

QY 79 VTAAYNMSFGEKLLPIWGKARPALDGLVGRALPATVHYRADGSVETAABEPLVPMAT 138
DB 80 VLVGFRAAFQDRLLPFPAKAGPALDGLVGRALPATVHYRADGSVETAABEPLVPMAT 139

QY 139 VVFQCVFAAITLLVAGSLIGRMSFLAMNIFVPLMTFSYTVGAFSLMG 198
DB 140 LVLFEEFAAITLVLAGSLIGRMSFLAMNIFVPLMTFSYTVGAFSLMG 199

QY 199 DYCGGYIHSVAGIAGTAAYWGPRAQKDRERPPNNILFTLTGAGLLMGNAGFVG 258
DB 200 DYSGGYIHLSSGAVGAAYWGPRAQKDRERPPNNILFTLTGAGLLMGNAGFVG 259

QY 259 PYAANS 264
DB 260 PYAANA 265

RESULT 12
US-10-953-349-17240
; Sequence 17240, Application US/10953349
; Publication No. US20060107345A1

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; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17240
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-17240

Query Match      34.8%; Score 881; DB 6; Length 218;
Best Local Similarity 72.5%; Pred. No. 1,9e-64;
Matches 158; Conservative 23; Mismatches 37; Indels 0; Gaps 0;

QY 44 VEGLVVVGKVKKKAANSAPALYAFPAWVICWVTMAVYNSFGEKLPIMGKAPALD 103
DB 1 MEGVLVLYSMVKKKAANSAPALYAFPAWVICWLVCHRMAGFDKLPFMGKAPALG 60
QY 104 QGLVGRALPATVHYRADGSVETAAVEBLYPMATVYFCVFAITLLIVAGSLGRMS 163
DB 61 QKFLTHRAKVPSESTHYNNGTVESATSEPLFATASLVFQFTFAITLLILAGSVLGRMN 120
QY 164 FLAMNIFVPLMTFTSTYVAFSLMGSGFLFHHGVIDYCGGYVIHVSAGIAGTAAVWVP 223
DB 121 IKAMMAFVPLMLFSTYVAFSLMGSGFLYHGWVIDYSGGYVIHLSGSIAGTAAVWVP 180
QY 224 RAQXDRERFPNNILFTLTGAGLLMWGMAGFNGGAPYA 261
DB 181 RLKSDRERFPNNVLLMLAGAGLLMWGMGSGFNGAPYA 218
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RESULT 13
US-10-953-349-17241
; Sequence 17241, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17241
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-17241
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Query Match      33.3%; Score 845; DB 6; Length 208;
Best Local Similarity 73.1%; Pred. No. 1.5e-61;
Matches 152; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 54 VYKKMAVNSAPALYAFPAWVICWVTMAVYNSFGEKLPIMGKAPALDQGLVGRAL 113
DB 1 MYKKMAVNSAPALYAFPAWVICWLVCHRMAGFDKLPFMGKAPALGQKFLTHRAKY 60
QY 114 PATVHYRADGSVETAAVEBLYPMATVYFCVFAITLLIVAGSLGRMSFLAMNIFVPL 173
DB 61 PESTHYNNGTVESATSEPLFATASLVFQFTFAITLLILAGSVLGRMNIRAMMAFVPL 120
QY 174 WLTFSYTVGAFSLMGSGFLFHHGVIDYCGGYVIHVSAGIAGTAAVWVPRAQXDRERFP 233
DB 121 WLFTSTYVAFSLMGSGFLYHGWVIDYSGGYVIHLSGSIAGTAAVWVPRKSDRERFP 180
QY 234 PNNILFTLTGAGLLMWGMAGFNGGAPYA 261
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DB 181 PNNVLLMLAGAGLLMWGMGSGFNGAPYA 208

RESULT 14
US-10-449-902-40126
; Sequence 40126, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40126
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-40126
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Query Match      30.3%; Score 769; DB 6; Length 219;
Best Local Similarity 69.0%; Pred. No. 2.4e-55;
Matches 140; Conservative 24; Mismatches 39; Indels 0; Gaps 0;

QY 19 SVADWLNGDNAMQVVAATLVGLQSPGLVYLYGGVKKKAANSAPALYAFPAWVICW 78
DB 16 AVPEWLNLDGNGMQVLAATFVGLQSPGLVLYGSIYKKKAANSAPALYASTLLVW 75
QY 79 VTMAYNSFGEKLPIMGKAPALDQGLVGRALPATVHYRADGSVETAAVEBLYPMAT 138
DB 76 VLVGRMAFGDRLPLFMGKAGALTEGFLVARSVPATVHVKDGLSPRTEPYPEAS 135
QY 139 VYFQCPAATLLIVAGSLGRMSFLAMNIFVPLMTFTSTYVAFSLMGSGFLFHHGVI 198
DB 136 WLFQFELAAITLVLAASLLGRMNKIKAMMAFTPLMLFSTYVCAFSLMGSGFLYQWGI 195
QY 199 DYCGGYVIHVSAGIAGTAAVWV 221
DB 196 DYSGGYVIHLSGSIAGTAAVWV 218
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RESULT 15
US-10-471-571A-244
; Sequence 244, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 244
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(428)
; OTHER INFORMATION: probabale ammonium
; US-10-471-571A-244
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